

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 1, 2004, 20:15:24 ; Search time 61 Seconds
(without alignments)

736.902 Million cell updates/sec

Title: US-09-648-310-2

Perfect score: 405

Sequence: 1 MNVEHVNLLVEETHRLGSK.....AGELLQGVHDDVDIVLLQD 81

Scoring table:

	BLOSUM62
Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delpop 6.0 , Delpext 7.0	

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgm2_1/USPTO_spool_p/US09648310/runat_27082004_154406_27960/app_query.fasta_1.526
-DB=Issued Patents NA -QMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -NATRX-blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pco -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09648310 @CGN 1 1 141 @runat_27082004_154406_27960 -NCPU=6 -ICPU=3
-NO MWAP -LARGQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:
1: /cgm2_6/ptodata/2/ina/5A.COMB.seq:*
2: /cgm2_6/ptodata/2/ina/5B.COMB.seq:*
3: /cgm2_6/ptodata/2/ina/6A.COMB.seq:*
4: /cgm2_6/ptodata/2/ina/6B.COMB.seq:*
5: /cgm2_6/ptodata/2/ina/PTCUS.COMB.seq:*
6: /cgm2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	368	90.6	800	4	US-09-644-460-26
2	351	86.5	786	4	US-09-023-655-79
3	67	16.5	1449	4	US-09-252-991A-13298
4	67	16.5	2028	4	US-09-252-991A-12500
5	67	16.5	2040	4	US-09-252-991A-12977
6	66.5	16.4	393	4	US-09-252-991A-12137
7	65	16.0	421	4	US-09-313-294A-4253
8	65	16.0	1664976	4	US-08-946-421B-1
9	64	15.8	2133	4	US-09-328-352-1774
10	63.5	15.6	1134	4	US-09-252-991A-8104
11	63.5	15.6	1314	4	US-09-252-991A-8001
12	63.5	15.6	1755	4	US-09-252-991A-8133

C 13	63	15.5	1038	4	US-09-252-991A-13643	Sequence 13643, A
C 14	63	15.5	1266	4	US-09-252-991A-13795	Sequence 13795, A
C 15	62.5	15.4	2323	1	US-08-358-901-1	Sequence 1, Appli
C 16	62.5	15.4	2323	1	US-08-566-347-1	Sequence 1, Appli
C 17	62.5	15.4	2323	1	US-08-693-835-1	Sequence 1, Appli
C 18	62	15.3	2329	1	US-08-457-797A-8	Sequence 8, Appli
C 19	62	15.3	2329	1	US-08-812-025-8	Sequence 8, Appli
C 20	62	15.3	2329	3	US-09-138-873A-8	Sequence 8, Appli
C 21	62	15.3	28958	1	US-08-358-261B-6	Sequence 6, Appli
C 22	62	15.3	28958	1	US-08-456-837-6	Sequence 6, Appli
C 23	62	15.3	28958	1	US-08-457-342-6	Sequence 6, Appli
C 24	62	15.3	28958	1	US-08-457-646A-6	Sequence 6, Appli
C 25	62	15.3	28958	1	US-08-458-076A-6	Sequence 6, Appli
C 26	62	15.3	28958	1	US-08-764-233A-4	Sequence 4, Appli
C 27	62	15.3	28958	1	US-08-457-335A-6	Sequence 6, Appli
C 28	62	15.3	28958	1	US-08-729-214-6	Sequence 6, Appli
C 29	62	15.3	28958	3	US-09-028-934-6	Sequence 6, Appli
C 30	62	15.3	49377	1	US-08-764-233A-1	Sequence 1, Appli
C 31	61.5	15.1	669	4	US-09-252-991A-4849	Sequence 4849, Ap
C 32	61.5	15.1	1008	4	US-09-252-991A-4906	Sequence 4906, Ap
C 33	61	15.0	885	4	US-09-328-352-1423	Sequence 1423, Ap
C 34	61	15.0	885	4	US-09-489-039A-3762	Sequence 3762, Ap
C 35	61	15.0	1278	4	US-09-134-000C-2571	Sequence 2571, Ap
C 36	61	15.0	1830121	4	US-09-557-884-1	Sequence 1, Appli
C 37	61	15.0	1830121	4	US-09-643-990A-1	Sequence 139, App
C 38	60	14.8	36800	4	US-08-311-731A-139	Sequence 1, Appli
C 39	60	14.8	640681	4	US-09-790-988-1	Sequence 6269, Ap
C 40	59.5	14.7	1419	4	US-09-252-991A-6269	Sequence 8717, Ap
C 41	59.5	14.7	1689	4	US-09-252-991A-8717	Sequence 6032, Ap
C 42	59.5	14.7	1965	4	US-09-252-991A-6032	Sequence 9230, Ap
C 43	59.5	14.7	1965	4	US-09-252-991A-9230	Sequence 188, App
C 44	59.5	14.7	2151	2	US-08-658-665-188	Sequence 41, Appl
C 45	59.5	14.7	2151	3	US-08-796-101-41	

ALIGNMENTS

RESULT 1
US-09-644-460-26
; Sequence 26, Application US/09644460
; Patent No. 6657053
; GENERAL INFORMATION:
; APPLICANT: Fisher, Paul B.
; TITLE OF INVENTION: Reciprocal Subtraction Differential
; TITLE OF INVENTION: Display
; FILE REFERENCE: 34587-C-PCT-USA
; CURRENT APPLICATION NUMBER: US/09/644,460
; CURRENT FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US99/04323
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: US 09/197,889
; PRIOR FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: US 09/185,115
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: US 09/032,684
; PRIOR FILING DATE: 1998-02-27
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 800
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-644-460-26

Alignment Scores:
Pred. No.: 1.61e-48 Length: 800
Score: 368.00 Matches: 79
Percent Similarity: 95.18% Conservative: 0
Best Local Similarity: 95.18% Mismatches: 2
Query Match: 90.64% Indels: 2
DB: 4 Gaps: 0

US-09-648-310-2 (1-81) x US-09-644-460-26 (1-800)

QY 1 MetAsnValGluHisGluValAsnLeuValGluGluHisArgLeuGlySerLys 20
 Db 170 ATGAACGTGGAGCATGAGGTTAACTCTCTGGTGGAGGAATTCATCGTCTGGTTCCAAA 229
 QY 21 AsnAlaAspGlyLysLeuSerValLysPheGlyValLeuPheGlnAspArgCysAla 40
 Db 230 AATGCCGATGGGAACACTGAGTGTGAAGTTTGGGGTCTCTTCCAGACGACAGATGTGCC 289
 QY 41 AsnLeuPheGluAla-LeuValGlyThrLeuLysAla-AlaLysArgArgLysIleValT 60
 Db 290 AATCTCTTTGAACCGTGTGGGAACTCTGAAGCCCGCAACGAGGAGATGTGTA 349
 QY 60 hTyrAlaGlyGluLeuLeuGlnGlyValHisAspValAspIleValLeuLeuG 80
 Db 350 CGTAGCAGAGAGCTGCTTTTGAAGGTGTTTCATGATGATGTTGACATTTGATTGCTGC 409
 QY 80 InAsp 81
 Db 410 AAGAT 414
 RESULT 2
 US-09-023-655-79
 ; Sequence 79, Application US/09023655
 ; Patent No. 6607879
 ; GENERAL INFORMATION:
 ; APPLICANT: Cocks, Benjamin G.
 ; APPLICANT: Susan G. Stuart
 ; APPLICANT: Jeffrey J. Seilhamer
 ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
 ; TITLE OF INVENTION: EXPRESSION
 ; NUMBER OF SEQUENCES: 1508
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 ; STREET: 3174 PORTER DRIVE
 ; CITY: PALO ALTO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/023,655
 ; FILING DATE: HEREWITH
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Zeller, Karen J.
 ; REGISTRATION NUMBER: 37,071
 ; REFERENCE/DOCKET NUMBER: PA-0001 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (650) 855-0555
 ; TELEFAX: (650) 845-4166
 ; INFORMATION FOR SEQ ID NO. 79:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 786 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: THP1PLB01
 ; CLONE: 012364
 ; US-09-023-655-79
 Alignment Scores: 7,48e-46 Length: 786
 Pred. No.: 351.00 Matches: 76
 Score:

Percent Similarity: 95.24% Conservative: 4
 Best Local Similarity: 90.48% Mismatches: 1
 Query Match: 86.45% Indels: 3
 DB: Gaps: 0
 US-09-648-310-2 (1-81) x US-09-023-655-79 (1-786)
 QY 1 MetAsnValGluHisGluValAsnLeuValGluGluHisArgLeuGlySerLys 20
 Db 140 ATGAATGTGATCAGGAGGTTAACTCTTAGTGGAGGAATTCATCGTTGGGTTCAAAA 199
 QY 21 AsnAlaAspGlyLysLeuSer-ValLys-PheGlyValLeuPheGlnAspArgCysAla 40
 Db 200 AATGCTGATGGAAGTTAAGCCGTGAATTTTGGGTCTCTTCCGTGATGATTAATGTC 259
 QY 40 laAsnLeuPheGluAlaLeuValGlyThrLeuLysAlaAla-LysArgArgLysIleVal 59
 Db 260 CCAACCTCTTTGAAGCATTTGGTAGGAACCTTTAAAGCTGCAAAAACGAAGGAGATTGTA 319
 QY 60 ThrTyrAlaGlyGluLeuLeuGlnGlyValHisAspValAspIleValLeuLeu 79
 Db 320 ACATATCCAGGAGAGCTGCTTCTGCAAGGTGTTTCATGATGATGTTGACATTATATTACGT 379
 QY 80 GlnAsp 81
 Db 380 CAAGAT 385
 RESULT 3
 US-09-252-991A-13298/c
 ; Sequence 13298, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 13298
 ; LENGTH: 1449
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas aeruginosa
 ; US-09-252-991A-13298
 Alignment Scores: 0.943 Length: 1449
 Pred. No.: 67.00 Matches: 32
 Score: 67.00 Conservative: 12
 Percent Similarity: 40.00% Mismatches: 32
 Best Local Similarity: 29.09% Indels: 34
 Query Match: 16.50% Gaps: 6
 DB:
 US-09-648-310-2 (1-81) x US-09-252-991A-13298 (1-1449)
 QY 3 ValGluHisGluValAsnLeuValGluGlu-----IleHis 15
 Db 1357 GTTGTCACGATGCGCGGTACACGCGGAGAACGCGTTGGCGGGAGCCGGCTTCAT 1298
 QY 16 ArgLeuGlySerLys-----AsnAlaAspGlyLysLeuSerValLysPheGly 31
 Db 1297 CGCGTGGCGCGCGCGGCGGTTCATCAGGAGGCGCGGTCTCGGTCTGCCACAGGT 1238
 QY 32 ValLeuPheGlnAspArgCysAlaAsnLeuPheGluAlaLeuValGlyThrLeuLys 51
 Db 1237 GTC-----GACGATCGGCGGCGGCGGCTCTGTAGTACACTGCCA 1187
 QY 52 AlaAlaLys-----ArgArgLysIleValThrTyrAlaGlyGluLeu--- 65
 Alignment Scores: 7,48e-46 Length: 786
 Pred. No.: 351.00 Matches: 76
 Score:

Db 1186 GGCCTCCGGTGTGATCGCTCGCCACCGAACCAGCAGCAGCGGTGGACCGTCGGC 1127
Qy 66 -----LeuLeuGlnGlyValHis----- 71
Db 1126 ACCGCCACCGCGCTTGCCTTCGGCCATCATCGCGGATCGCGTTCGGCGGGTGTGA 1067
Qy 72 AspAspValAspIleValLeuLeuGlnAsp 81
Db 1066 GAGGATGTTGACCTTGCTTGCTGTGATGAT 1037
RESULT 4
US-09-252-991A-12500
; Sequence 12500, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 12500
; LENGTH: 2028
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12500
Alignment Scores:
Pred. No.: 1.52 Length: 2028
Score: 67.00 Matches: 32
Percent Similarity: 40.00% Conservative: 12
Best Local Similarity: 29.09% Mismatches: 32
Query Match: 16.50% Indels: 34
DB: 4 Gaps: 6
US-09-648-310-2 (1-81) x US-09-252-991A-12500 (1-2028)
Qy 3 ValGluHisGluValAsnLeuValGluGlu-----IleHis 15
Db 655 GTTGTCACCGAGTGGCGGTACACGCCGGAAGACGGTGTGGCGGAGCGCGCTTCAT 714
Qy 16 ArgLeuGlySerLys-----AsnAlaAspGlyLysLeuSerValLysPheGly 31
Db 715 CGCGTGGCGCGCGCGCGGTATCAGCAGCGCGCGGTCTCGGTCTGCCACCGGT 774
Qy 32 ValLeuPheGlnAspAspArgCysAlaAsnLeuPheGluAlaLeuValGlyThrLeuLys 51
Db 775 GTC-----GACGATCGGCGCAGCGCGACTGGCGGCGGTCTCGTAGTACCACTGCCA 825
Qy 52 AlaAlaLys-----ArgArgLysIleValThrTyralaGlyGluLeu--- 65
Db 826 GGCCTCCGGTGTGATCGCTCGCCACCGAACCAGCAGCAGCGGTGGACCGTCGGC 885
Qy 66 -----LeuLeuGlnGlyValHis----- 71
Db 886 ACCGCCACCGCGCTTGCCTTCGGCCATCATCGCGGATCGCGTTCGGCGGGTGTGA 945
Qy 72 AspAspValAspIleValLeuLeuGlnAsp 81
Db 946 GAGGATGTTGACCTTGCTTGCTGTGATGAT 975
RESULT 5
US-09-252-991A-12977/c
; Sequence 12977, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 12977
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12977
Alignment Scores:
Pred. No.: 1.53 Length: 2040
Score: 67.00 Matches: 32
Percent Similarity: 40.00% Conservative: 12
Best Local Similarity: 29.09% Mismatches: 32
Query Match: 16.50% Indels: 34
DB: 4 Gaps: 6
US-09-648-310-2 (1-81) x US-09-252-991A-12977 (1-2040)
Qy 3 ValGluHisGluValAsnLeuValGluGlu-----IleHis 15
Db 1437 GTTGTCACCGAGTGGCGGTACACGCCGGAAGACGGTGTGGCGGAGCGCGCTTCAT 1378
Qy 16 ArgLeuGlySerLys-----AsnAlaAspGlyLysLeuSerValLysPheGly 31
Db 1377 CGCGTGGCGCGCGCGCGGTATCAGCAGCGCGCGGTCTCGGTCTGCCACCGGT 1318
Qy 32 ValLeuPheGlnAspAspArgCysAlaAsnLeuPheGluAlaLeuValGlyThrLeuLys 51
Db 1317 GTC-----GACGATCGGCGCAGCGCGACTGGCGGCGGTCTCGTAGTACCACTGCCA 1267
Qy 52 AlaAlaLys-----ArgArgLysIleValThrTyralaGlyGluLeu--- 65
Db 1266 GGCCTCCGGTGTGATCGCTCGCCACCGAACCAGCAGCAGCGGTGGACCGTCGGC 1207
Qy 66 -----LeuLeuGlnGlyValHis----- 71
Db 1206 ACCGCCACCGCGCTTGCCTTCGGCCATCATCGCGGATCGCGTTCGGCGGGTGTGA 1147
Qy 72 AspAspValAspIleValLeuLeuGlnAsp 81
Db 1146 GAGGATGTTGACCTTGCTTGCTGTGATGAT 1117
RESULT 6
US-09-252-991A-12137
; Sequence 12137, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 12137
; LENGTH: 393
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12137
Alignment Scores:
Pred. No.: 0.178 Length: 393

Score: 66.50 Matches: 23
Percent Similarity: 43.21% Conservative: 12
Best Local Similarity: 28.40% Mismatches: 35
Query Match: 16.38% Indels: 11
DB: 4 Gaps: 3

US-09-648-310-2 (1-81) x US-09-252-991A-12137 (1-393)

QY 1 MetAsnValGluHisGluValAsnLeuValGluGluLeuHisArgLeuGlySerIys 20
DB 136 ATGAAGCGCACACAGCACTCAACCCATCCGATCTCGTGAAGCGCTG-----AAA 189
QY 21 AsnAlaAspGlyLysLeuSerValLysPheGlyValLeuPheGlnAspArgCysAla 40
DB 190 CGCGCGGATGGTCACTCTTCGGCACGCTCATAGGGATGCAAAAGTGGCGAATCTGCTC 249
QY 41 AsnLeuPheGluAlaLeuValGlyThrLeuLysAlaAlaLysArgArgLysIleValThr 60
DB 250 GACATCGCCGCGCAGCTCGCGCGGTGGAAGCGG-----GTGACG 291
QY 61 TyrAlaGlyGluLeuLeuGlnGlyValHisAspValAspValAspIleValLeuGln 80
DB 292 GCCGCAAGCGGCTCTG-----ATCCAGCACACATCGACCATTCGCTGCGCCAT 342
QY 81 Asp 81
DB 343 GAC 345

RESULT 7

US-09-313-294A-4253/c
; Sequence 4253 Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1993-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 4253
; LENGTH: 421
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. 6476212 700348078H1
; LOCATION: 14, 266, 310, 315, 317, 410, 414
; OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-4253

Alignment Scores:
Pred. No.: 0.337 Length: 421
Score: 65.00 Matches: 24
Percent Similarity: 46.88% Conservative: 6
Best Local Similarity: 37.50% Mismatches: 24
Query Match: 16.01% Indels: 10
DB: 4 Gaps: 3

US-09-648-310-2 (1-81) x US-09-313-294A-4253 (1-421)

QY 2 AsnValGluHisGluValAsnLeuValGluGluLeuHisArgLeu----- 17
DB 219 AATCTTGACACGCGCGGCTCTCTCGTAGATGAACCCGAGATCGCTTGACGCGC 160
QY 18 ---GlySerLysAsnAlaAspGlyLysLeuSerValLysPheGlyValLeuPheGlnAsp 36
DB 159 CCTTCTTCGCCAACTCGGATCGCGGCTTGTGTGATGCCCTGGATGTTGTCAACGAC 100
QY 37 AspArgCysAlaAsnLeuPheGluAlaLeuValGlyThr-----LeuLysAlaAla 53

DB 99 TTGCGGTGGCT-----TGCGCGCGCTTGGCCAGACCTTCCCGCCCTTCCCGCGGCC 46
QY 54 LysArgArgLys 57
DB 45 AGACATCGCGCA 34

RESULT 8

US-08-916-421B-1/c
; Sequence 1, Application US/08916421B
; Patent No. 6503729
; GENERAL INFORMATION:
; APPLICANT: Bult et al.
; TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococcus
; TITLE OF INVENTION: jannaschii
; FILE REFERENCE: PB275
; CURRENT APPLICATION NUMBER: US/08/916,421B
; CURRENT FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: US 60/024,428
; PRIOR FILING DATE: 1996-08-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 1664976
; TYPE: DNA
; ORGANISM: Methanococcus jannaschii
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (28222)..(28222)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc.feature
; LOCATION: (28257)..(28258)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc.feature
; LOCATION: (84773)..(84773)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc.feature
; LOCATION: (84808)..(84808)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc.feature
; LOCATION: (84812)..(84812)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc.feature
; LOCATION: (98120)..(98120)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc.feature
; LOCATION: (98159)..(98159)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc.feature
; LOCATION: (98239)..(98239)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc.feature
; LOCATION: (98266)..(98266)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc.feature
; LOCATION: (98343)..(98343)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc.feature
; LOCATION: (103998)..(103998)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc.feature
; LOCATION: (148948)..(148948)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc.feature
; LOCATION: (163385)..(163385)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc.feature
; LOCATION: (191989)..(191989)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc.feature
; LOCATION: (191995)..(191995)
; OTHER INFORMATION: n equals a, t, c, or g

NAME/KEY: misc feature
LOCATION: (231580)..(231980)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (234187)..(234187)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (234220)..(234220)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (234814)..(234814)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (309398)..(309398)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (309418)..(309418)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (312837)..(312837)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (312993)..(312993)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (319226)..(319226)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (559167)..(559167)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (559241)..(559241)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (600992)..(600992)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (622708)..(622708)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (657081)..(657081)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (657203)..(657203)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (674435)..(674435)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (682442)..(682442)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (713652)..(713652)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (741684)..(741684)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (779455)..(779455)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (779676)..(779676)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (855539)..(855539)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (871619)..(871619)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1084830)..(1084830)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature

LOCATION: (1096846)..(1096846)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1119881)..(1119881)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1130881)..(1130881)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1310988)..(1310988)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1313224)..(1313224)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1349473)..(1349473)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1349491)..(1349491)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1470091)..(1470091)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1569020)..(1569020)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1602912)..(1602912)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1603734)..(1603734)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1637998)..(1637998)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1664854)..(1664854)
OTHER INFORMATION: n equals a, t, c, or g
US-08-916-421B-1

Alignment Scores: 4.22e+04 Length: 1664976
Pred. No.: 65.00 Matches: 18
Score: 49.25% Conservative: 15
Best Local Similarity: 26.87% Mismatches: 20
Query Match: 16.01% Indels: 14
DB: 4 Gaps: 3

US-09-648-310-2 (1-81) x US-08-916-421B-1 (1-1664976)

Qy 3 ValGluHisGluValAsn-----LeuLeuValGluGluLeuHisArgLeuGlySer 19
Db 720607 ATTGAGCATAGGTTAGAGATGCCCTTTTGTGTCAGAAATGCTAATGCCGTGCT--- 720551
Qy 20 LysAsnAlaAspGlyLysLeuSerValLysPheGlyValLeuPheGlnAspArgCys 39
Db 720550 -----AGAAATGCTTATTGCTAGGTATTGGAATCTGCTTAGAAGATGATGAATGC 720497
Qy 40 AlaAsnLeu-----PheGluAlaLeuValGlyThrLeuLys 51
Db 720496 ATAAAGATAGGTAATCAATCCATGGAGTATATAAAGAACTTAATCAATGAACCTTAA 720437
Qy 52 AlaAlaLysArgGlyLys 58
Db 720436 AGTGTTAACTAAAAAATTA 720416

RESULT 9

US-09-328-352-1774
; Sequence 1774, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

;; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

;; FILE REFERENCE: GTC99-03PA

;; CURRENT APPLICATION NUMBER: US/09/328,352

;; CURRENT FILING DATE: 1999-06-04

;; NUMBER OF SEQ ID NOS: 8252

;; SEQ ID NO 1774

;; LENGTH: 2133

;; TYPE: DNA

;; ORGANISM: Acinetobacter baumannii

US-09-328-352-1774

Alignment Scores:

Pred. No.:	4.85	Length:	2133
Score:	64.00	Matches:	21
Percent Similarity:	53.03%	Conservative:	14
Best Local Similarity:	31.82%	Mismatches:	23
Query Match:	15.76%	Indels:	8
DB:	4	Gaps:	4

US-09-648-310-2 (1-81) x US-09-328-352-1774 (1-2133)

QY	1	MetAsnValGluHisGluValAsnLeuValGluGluIleHisArgLeuGlySerLys	20
DB	1396	ATGGTGGTACGGCGTGAACACAACTGGTGCCTTATGTCAT---TTAGGAACGGGT	1452
QY	21	Asn-----AlaAspGlyLysLeuSerValLysPheGlyValLeuPheGlnAsp---	36
DB	1453	AACTACCATGCTATGATGCTGCATTTATCTACTGATTACGGCCTAATGACCACCGATAAA	1512
QY	37	AspArgCysAlaAsn-----LeuPheGluAlaLeuValGlyThrLeuLysAlaAla	53
DB	1513	GACTGTGTGAAGACGTACACCGTATTTTCCAGAGCTCACGGGTATGGGTAAATGGCA	1572
QY	54	LysArgArgLysIleVal	59
DB	1573	AAACTGAAAAAGTTACTC	1590

RESULT 10

US-09-252-991A-8104/c

;; Sequence 8104, Application US/09252991A

;; Patent No. 6551795

;; GENERAL INFORMATION:

;; APPLICANT: Marc J. Rubenfield et al.

;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

;; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

;; FILE REFERENCE: 107196.136

;; CURRENT APPLICATION NUMBER: US/09/252,991A

;; CURRENT FILING DATE: 1999-02-18

;; PRIOR APPLICATION NUMBER: US 60/074,788

;; PRIOR FILING DATE: 1998-02-18

;; PRIOR APPLICATION NUMBER: US 60/094,190

;; PRIOR FILING DATE: 1998-07-27

;; NUMBER OF SEQ ID NOS: 33142

;; SEQ ID NO 8104

;; LENGTH: 1134

;; TYPE: DNA

;; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-8104

Alignment Scores:

Pred. No.:	2.37	Length:	1134
Score:	63.50	Matches:	26
Percent Similarity:	41.03%	Conservative:	6
Best Local Similarity:	33.33%	Mismatches:	21
Query Match:	15.64%	Indels:	25
DB:	4	Gaps:	4

US-09-648-310-2 (1-81) x US-09-252-991A-8104 (1-1134)

QY	14	IleHisArgLeuGlySerLysAsnAlaAspGlyLysLeuSerValLysPheGlyValLeu	33
----	----	--	----

DB	775	GTTTCATCGC-----CAGCGCGATGGGAACCTGCCGCGAGTCTTCGCGGTAGAC	728
----	-----	--	-----

QY	34	PheGlnAspArgCysAlaAsnLeuPheGluAlaLeu-----	46
DB	727	GCGATGATCGACAGGGTGCCGCCCTTGCCAGGCCCTGCACGCCCACTCCAGGCGCTG	668
QY	47	-----ValGlyThrLeuLysAlaAlaLysArgArgLysIle	58
DB	667	TGCGGGGGCGTTGCCGGGACTCCAGCTGCTGCTCTCTGCGCGCGCGCGGT-----	614
QY	59	ValThrTyrAlaGlyGluLeuLeuGlnGlyValHis---AspAspValAsp	75
DB	613	-----GGCGGTGCCATGCTGTCTCGCGCTCCACGCCGACGCGTGCAT	569

RESULT 11

US-09-252-991A-8001/c

;; Sequence 8001, Application US/09252991A

;; Patent No. 6551795

;; GENERAL INFORMATION:

;; APPLICANT: Marc J. Rubenfield et al.

;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

;; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

;; FILE REFERENCE: 107196.136

;; CURRENT APPLICATION NUMBER: US/09/252,991A

;; CURRENT FILING DATE: 1999-02-18

;; PRIOR APPLICATION NUMBER: US 60/074,788

;; PRIOR FILING DATE: 1998-02-18

;; PRIOR APPLICATION NUMBER: US 60/094,190

;; PRIOR FILING DATE: 1998-07-27

;; NUMBER OF SEQ ID NOS: 33142

;; SEQ ID NO 8001

;; LENGTH: 1314

;; TYPE: DNA

;; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-8001

Alignment Scores:

Pred. No.:	2.92	Length:	1314
Score:	63.50	Matches:	26
Percent Similarity:	41.03%	Conservative:	6
Best Local Similarity:	33.33%	Mismatches:	21
Query Match:	15.64%	Indels:	25
DB:	4	Gaps:	4

US-09-648-310-2 (1-81) x US-09-252-991A-8001 (1-1314)

QY	14	IleHisArgLeuGlySerLysAsnAlaAspGlyLysLeuSerValLysPheGlyValLeu	33
DB	1023	GTTTCATCGC-----CAGCGCGATGGGAACCTGCCGCGAGTCTTCGCGGTAGAC	976
QY	34	PheGlnAspArgCysAlaAsnLeuPheGluAlaLeu-----	46
DB	975	GCGATGATCGACAGGGTGCCGCCCTTGCCAGGCCCTGCACGCCCACTCCAGGCGCTG	916
QY	47	-----ValGlyThrLeuLysAlaAlaLysArgArgLysIle	58
DB	915	TGCGGGGGCGTTGCCGGGACTCCAGCTGCTGCTCTCTGCGCGCGCGCGGT-----	862
QY	59	ValThrTyrAlaGlyGluLeuLeuGlnGlyValHis---AspAspValAsp	75
DB	861	-----GGCGGTGCCATGCTGTCTCGCGCTCCACGCCGCGCGGTGCAT	817

RESULT 12

US-09-252-991A-8133

;; Sequence 8133, Application US/09252991A

;; Patent No. 6551795

;; GENERAL INFORMATION:

;; APPLICANT: Marc J. Rubenfield et al.

;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

;; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

;; FILE REFERENCE: 107196.136

;; CURRENT APPLICATION NUMBER: US/09/252,991A

;; CURRENT FILING DATE: 1999-02-18

;; PRIOR APPLICATION NUMBER: US 60/074,788

;; PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 8133
LENGTH: 1755
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-8133

Alignment Scores:
Pred. No.: 4.4 Length: 1755
Score: 63.50 Matches: 26
Percent Similarity: 41.03% Conservative: 6
Best Local Similarity: 33.33% Mismatches: 21
Query Match: 15.64% Indels: 25
DB: 4 Gaps: 4

US-09-648-310-2 (1-81) x US-09-252-991A-8133 (1-1755)

Qy 14 lIeHisArgLeuGlySerLysAsnAlaAspGlyLysLeuSerValLysPheGlyValLeu 33
Db 1279 GTTCATGCG-----CAGGCCGATGGGAACCTGCGCGAGTCTTCGGCGTAGAC 1326

Qy 34 PheGlnAspAspArgCysAlaAsnLeuPheGluAlaLeu----- 46
Db 1327 GCCGATGATCGACAGAGGTGCGCGCTTGCCGCGGCCCTTGACCCGCCACTCCAGGGCGCTG 1386

Qy 47 -----ValGlyThrLeuLysAlaAlaLysArgArgLysIle 58
Db 1387 TCGCGGGCGGTGCGGGACTCCAGTGTGCTCTGCGCGCGCGCGGT----- 1440

Qy 59 ValThrTyrAlaGlyGluLeuLeuGlnGlyValHis---AspAspValAsp 75
Db 1441 -----GCGGTGTCATGCTGTGTCGCGCGTCCACGCCGCGCGGTGAT 1485

RESULT 13
US-09-252-991A-13643/c
Sequence 13643, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 13643
LENGTH: 1038
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13643

Alignment Scores:
Pred. No.: 2.51 Length: 1038
Score: 63.00 Matches: 18
Percent Similarity: 64.10% Conservative: 7
Best Local Similarity: 46.15% Mismatches: 8
Query Match: 15.52% Indels: 6
DB: 4 Gaps: 2

US-09-648-310-2 (1-81) x US-09-252-991A-13643 (1-1038)

Qy 42 LeuPheGluAlaLeuValGlyThrLeuLysAlaAlaLysArgArgLysIleValThrTyr 61
Db 720 CTTTCCCGCGCTTCTCGGTGTTCTC---GCCGAATACCGTACGCTGCTTCTTCA 664

Qy 62 AlaGlyGluLeuLeuGlnGlyValHisAspAspValAspIleValLeuLeuGln 80

Db 62 CTTTCCCGCGCTTCTCGGTGTTCTC---GCCGAATACCGTACGCTGCTTCTTCA 522

Db 663 GCCGGC-----GGTAAGCACCTCGAAGTCAATATCGTCTTCTTCAA 622

RESULT 14
US-09-252-991A-13795
Sequence 13795, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 13795
LENGTH: 1266
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13795

Alignment Scores:
Pred. No.: 3.32 Length: 1266
Score: 63.00 Matches: 18
Percent Similarity: 64.10% Conservative: 7
Best Local Similarity: 46.15% Mismatches: 8
Query Match: 15.52% Indels: 6
DB: 4 Gaps: 2

US-09-648-310-2 (1-81) x US-09-252-991A-13795 (1-1266)

Qy 42 LeuPheGluAlaLeuValGlyThrLeuLysAlaAlaLysArgArgLysIleValThrTyr 61
Db 424 CTTTCCCGCGCTTCTCGGTGTTCTC---GCCGAATACCGTACGCTGCTTCTTCA 480

Qy 62 AlaGlyGluLeuLeuGlnGlyValHisAspAspValAspIleValLeuLeuGln 80
Db 481 GCCGGC-----GGTAAGCACCTCGAAGTCAATATCGTCTTCTTCAA 522

RESULT 15
US-08-358-901-1/c
Sequence 1, Application US/08358901
Patent No. 5554521
GENERAL INFORMATION:
APPLICANT: Suslow, Trevor V.
APPLICANT: Jones, Jonathan D.G.
TITLE OF INVENTION: No. 5554521el Chitinase-Producing Plants
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,901
FILING DATE: 19-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/550,253
FILING DATE: 09-JUL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/888,033
FILING DATE: 18-JUL-1986

```
; * PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/593,691
; FILING DATE: 26-MAR-1984
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 12176-5-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2323 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 361..2043
;
US-08-358-901-1

Alignment Scores:
Pred. No.: 9.42 Length: 2323
Score: 62.50 Matches: 19
Percent Similarity: 52.94% Conservative: 17
Best Local Similarity: 27.94% Mismatches: 31
Query Match: 15.39% Indels: 1
DB: 1 Gaps: 1

US-09-648-310-2 (1-81) x US-08-358-901-1 (1-2323)
QY 5 HisGluValAsnLeuValGluGluIleHisArgLeuGlySerLysAsnAlaAspGly 24
Db 1086 CACGCCCTTCTCGGCTTTTGACGCGCGACGATCGTGGATCGAGATTGAA--- 1030
QY 25 LysLeuSerValLysPheGlyValLeuPheGlnAspArgCysAlaAsnLeuPheGlu 44
Db 1029 GTCTCGCGGCTTGGCAGGAGCGCTGCAAGCCTGGAAGCTGCTTCAATCTCTTCAG 970
QY 45 AlaLeuValGlyThrLeuLysAlaAlaLysArgLysIleValThrTyAlaGlyGlu 64
Db 969 GCTGCTGTGATGCGCATTCGCCCGCCAGATCGGATAAAGCCGTACACAGGTGGTCAG 910
QY 65 LeuLeuLeuGlnGlyValHisAsp 72
Db 909 GTTTGCGCGGGATCTTGTGCAC 886
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Search completed: September 1, 2004, 22:11:22
Job time : 233 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 1, 2004, 21:55:40 ; Search time 263.5 Seconds
(without alignments)
1512.848 Million cell updates/sec

Title: US-09-648-310-2
Perfect score: 406
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Delop 6.0 , Delext 7.0

Searched: 3237270 seqs, 2460713050 residues

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Maximum Match 100%
Listing first 45 summaries

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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.:	Score	Query Match	Length	ID	Description
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ALIGNMENTS

RESULT 1

US-10-373-556-1
; Sequence 1, Application US/10373556
; Publication No. US20030224402A1
; GENERAL INFORMATION:
; APPLICANT: Paul B. Fisher
; APPLICANT: Dong-chul Kang
; APPLICANT: Zao-Zhong Su
; TITLE OF INVENTION: PROGRESSION SUPPRESSED GENE 13 (PSGen13)
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: A34586-A-PCT-USA (070050.2305)
; CURRENT APPLICATION NUMBER: US/10/373,556
; CURRENT FILING DATE: 2003-02-24
; PRIOR FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: PCT/US01/26795
; PRIOR FILING DATE: 2000-08-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 780
; TYPE: DNA
; ORGANISM: rattus norvegicus

1	406	100.0	780	13	US-10-373-556-1	Sequence 1, Appli
2	406	100.0	780	13	US-10-373-556-5	Sequence 5, Appli
3	390	96.1	400	13	US-10-085-783A-21733	Sequence 21733, A
4	390	96.1	400	16	US-10-242-535A-21733	Sequence 21733, A
5	390	96.1	483	13	US-10-085-783A-56189	Sequence 56189, A
6	390	96.1	483	16	US-10-242-535A-56189	Sequence 56189, A
7	390	96.1	527	12	US-09-969-034-557	Sequence 557, App
8	390	96.1	778	9	US-09-925-300-557	Sequence 545, App
9	390	96.1	835	13	US-10-373-556-3	Sequence 3, Appli
10	390	96.1	835	13	US-10-373-556-6	Sequence 6, Appli
11	390	96.1	876	13	US-10-342-887-156	Sequence 156, App
12	390	96.1	876	13	US-10-172-118-156	Sequence 156, App
13	386	95.1	594	12	US-09-969-034-750	Sequence 750, App
14	384	94.6	717	12	US-09-969-034-748	Sequence 748, App
15	368	90.6	458	10	US-09-918-995-36075	Sequence 36075, A
16	368	90.6	800	17	US-10-725-969A-26	Sequence 26, Appli
17	351	86.5	786	17	US-10-641-643-79	Sequence 79, Appli
18	302	74.4	533	13	US-10-425-114-19867	Sequence 19867, A
19	286	70.4	486	9	US-09-938-842A-355	Sequence 355, App
20	286	70.4	486	11	US-09-938-842A-355	Sequence 355, App
21	286	70.4	492	10	US-09-770-961-318	Sequence 618, App
22	282	69.5	818	17	US-10-437-963-43648	Sequence 43648, A
23	272	67.0	716	13	US-10-424-599-94878	Sequence 94878, A
24	237	58.4	268	9	US-09-294-093B-2020	Sequence 2020, Ap
25	236	58.1	552	9	US-09-920-300A-939	Sequence 939, App
26	236	58.1	552	14	US-10-033-528-939	Sequence 939, App
27	236	58.1	552	15	US-10-093-926-939	Sequence 939, App
28	208	51.2	388	9	US-09-925-293-318	Sequence 318, App
29	208	51.2	388	10	US-09-925-299-318	Sequence 318, App
30	158	38.9	289	9	US-09-294-093B-4150	Sequence 4150, Ap
31	113	27.8	388	16	US-10-191-803-820	Sequence 820, App
32	109	26.8	1128	17	US-10-644-659A-3	Sequence 3, Appli
33	106	26.1	1146	17	US-10-644-659A-1	Sequence 1, Appli
34	106	26.1	1322	16	US-10-104-047-1199	Sequence 1199, Ap
35	98	24.1	60	10	US-09-908-975-22102	Sequence 22102, A
36	96.5	23.8	489	17	US-10-644-659A-7	Sequence 7, Appli
37	89	21.9	175	9	US-09-294-093B-5438	Sequence 5438, Ap
38	72.5	17.9	2960	17	US-10-437-963-34365	Sequence 34365, A
39	71	17.5	1728	13	US-10-282-132A-16022	Sequence 16022, A
40	69.5	17.1	1284	13	US-10-282-132A-39648	Sequence 39648, A
41	69.5	17.1	3806	13	US-09-854-867-62	Sequence 62, Appli
42	68.5	16.9	1107	13	US-10-425-114-33343	Sequence 33343, A
43	68.5	16.9	1257	13	US-10-282-122A-14898	Sequence 14898, A
44	68.5	16.9	2163	13	US-10-425-114-30828	Sequence 30828, A
45	66	16.3	321491	13	US-10-087-192-532	Sequence 532, App


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; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 56189
; LENGTH: 483
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-56189

Alignment Scores:
Pred. No.: 7,97e-54 Length: 483
Score: 390.00 Matches: 76
Percent Similarity: 98.77% Conservative: 4
Best Local Similarity: 93.83% Mismatches: 1
Query Match: 96.06% Indels: 0
DB: 16 Gaps: 0

US-09-648-310-2 (1-81) x US-10-242-535A-56189 (1-483)

QY 1 MetAsnValGluHisGluValAsnLeuValGluGluLeuHisArgLeuGlySerLys 20
Db 81 ATGAATGTGGATCAGGAGTTAACTCTTAGTGGAGGAAATTCATCGTTGGGTTCAAAA 140
QY 21 AsnAlaAspGlyLysLeuSerValLysPheGlyValLeuPheGlnAspArgCysAla 40
Db 141 AATGCTGATGGAAGTTAAGCTGAAATTTGGGCTCTTCGTTGATGATAATGTGCC 200
QY 41 AsnLeuPheGluAlaLeuValGlyThrLeuLysAlaAlaLysArgGlyLysLeuValThr 60
Db 201 AACCTCTTTGAAGCATTGTTAGGAACTCTTAAGCTGCAAAACGAAGGATTGTAACA 260
QY 61 TyrAlaGlyGluLeuLeuGlnGlyValHisAspValAspValLeuValLeuGln 80
Db 261 TATCCAGGAGAGCTGCTTCGCAAGGTTCATGATGATGATGATGATGATGATGATGCA 320
QY 81 Asp 81
Db 321 GAT 323

RESULT 7
US-09-969-034-557/c
; Sequence 557, Application US/09969034
; Publication No. US20040110668A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Astle, Jon H.
; APPLICANT: Carroll, Eddie III
; APPLICANT: Catino, Theodore J.
; APPLICANT: Dwivedi, Poorima
; APPLICANT: Molino, Gary A.
; APPLICANT: Thiasalingam, Arunthathi
; APPLICANT: Lewis, Marcia E.
; TITLE OF INVENTION: Nucleic Acid Sequences Differentially
; FILE REFERENCE: 1657/1032
; CURRENT APPLICATION NUMBER: US/09/969,034
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/237,271
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 4494
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 557
; LENGTH: 627
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 503-512, 539, 596, 620
; OTHER INFORMATION: n = A,T,C or G

US-09-969-034-557
Alignment Scores:
Pred. No.: 1.17e-53 Length: 627
Score: 390.00 Matches: 76
Percent Similarity: 98.77% Conservative: 4
Best Local Similarity: 93.83% Mismatches: 1
Query Match: 96.06% Indels: 0
DB: 12 Gaps: 0

US-09-648-310-2 (1-81) x US-09-969-034-557 (1-627)

QY 1 MetAsnValGluHisGluValAsnLeuValGluGluLeuHisArgLeuGlySerLys 20
Db 271 ATGAATGTGGATCAGGAGTTAACTCTTAGTGGAGGAAATTCATCGTTGGGTTCAAAA 212
QY 21 AsnAlaAspGlyLysLeuSerValLysPheGlyValLeuPheGlnAspArgCysAla 40
Db 211 AATGCTGATGGAAGTTAAGCTGAAATTTGGGCTCTTCGTTGATGATAATGTGCC 152
QY 41 AsnLeuPheGluAlaLeuValGlyThrLeuLysAlaAlaLysArgGlyLysLeuValThr 60
Db 151 AACCTCTTTGAAGCATTGTTAGGAACTCTTAAGCTGCAAAACGAAGGATTGTAACA 92
QY 61 TyrAlaGlyGluLeuLeuGlnGlyValHisAspValAspValLeuValLeuGln 80
Db 91 TATCCAGGAGAGCTGCTTCGCAAGGTTCATGATGATGATGATGATGATGATGATGCA 32
QY 81 Asp 81
Db 31 GAT 29

RESULT 8
US-09-925-300-545
; Sequence 545, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 545
; LENGTH: 778
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (641)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (652)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-300-545

Alignment Scores:
Pred. No.: 1.61e-53 Length: 778
Score: 390.00 Matches: 76
Percent Similarity: 98.77% Conservative: 4
Best Local Similarity: 93.83% Mismatches: 1
Query Match: 96.06% Indels: 0
DB: 9 Gaps: 0

US-09-648-310-2 (1-81) x US-09-925-300-545 (1-778)

QY 1 MetAsnValGluHisGluValAsnLeuValGluGluLeuHisArgLeuGlySerLys 20
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186 ATGAATGTGGATCAGAGGTTAACTCTTTAGTGAGGAAATTCATCGTTTGGGTTCAAAA 245
21 AsnAlaaspGlyLysLeuSerVallyspPheGlyValLeuPheGlnAspAspArgCysAla 40
246 AATGCTGATGGAAGTTAAGCGTGAATTTGGGTCCTCTTCGCTGATGATAAATGTGCC 305
41 AsnLeuPheGluAlaLeuValGlyThrLeuLysAlaAlaLysArgArgLysIleValThr 60
306 AACCTCTTTGAAGCATTTGTAAGCACTTTAAAGCTGCAAAACGAAAGAGATTGTAAAC 365
61 TyrAlaGlyGluLeuLeuGlnGlyValHisAspValAspIleValLeuGln 80
366 TATCCAGGAGAGCTGCTTCTGCAAGGTTCATCATGATGATTTGACATTATATTACTGCAA 425
81 Asp 81
426 GAT 428

RESULT 9
US-10-373-556-3
; Sequence 3, Application US/10373556
; Publication No. US20030224402A1
; GENERAL INFORMATION:
; APPLICANT: Paul B. Fisher
; APPLICANT: Dong-chul Kang
; APPLICANT: Zao-Zhong Su
; TITLE OF INVENTION: PROGRESSION SUPPRESSED GENE 13 (PSGen13)
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: A34586-A-PCT-USA (070050.2305)
; CURRENT APPLICATION NUMBER: US/10/373,556
; CURRENT FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: PCT/US01/26795
; PRIOR FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: 09/648,310
; PRIOR FILING DATE: 2000-08-25
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 835
; TYPE: DNA
; ORGANISM: homo sapiens
; APPLICANT: Paul B. Fisher
; APPLICANT: Dong-chul Kang
; APPLICANT: Zao-Zhong Su
; TITLE OF INVENTION: PROGRESSION SUPPRESSED GENE 13 (PSGen13)
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: A34586-A-PCT-USA (070050.2305)
; CURRENT APPLICATION NUMBER: US/10/373,556
; CURRENT FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: PCT/US01/26795
; PRIOR FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: 09/648,310
; PRIOR FILING DATE: 2000-08-25
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 835
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-373-556-3

Alignment Scores:
Pred. No.: 1.78e-53 Length: 835
Score: 390.00 Matches: 76
Percent Similarity: 98.77% Conservative: 4
Best Local Similarity: 93.83% Mismatches: 1
Query Match: 96.06% Indels: 0
DB: 13 Gaps: 0

US-09-648-310-2 (1-81) x US-10-373-556-3 (1-835)
Qy 1 MetAsnValGluHisGluValAsnLeuValGluGluLeuHisArgLeuGlySerLys 20
Db 197 ATGAATGTGGATCAGAGGTTAACTCTTTAGTGAGGAAATTCATCGTTTGGGTTCAAAA 256
21 AsnAlaaspGlyLysLeuSerVallyspPheGlyValLeuPheGlnAspAspArgCysAla 40
Db 257 AATGCTGATGGAAGTTAAGCGTGAATTTGGGTCCTCTTCGCTGATGATAAATGTGCC 316
41 AsnLeuPheGluAlaLeuValGlyThrLeuLysAlaAlaLysArgArgLysIleValThr 60
Db 317 AACCTCTTTGAAGCATTTGTAAGCACTTTAAAGCTGCAAAACGAAAGAGATTGTAAAC 376
61 TyrAlaGlyGluLeuLeuGlnGlyValHisAspValAspIleValLeuGln 80
Db 377 TATCCAGGAGAGCTGCTTCTGCAAGGTTCATCATGATGATTTGACATTATATTACTGCAA 436
81 Asp 81
437 GAT 439

RESULT 11
US-10-342-887-156
; Sequence 156, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
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186 ATGAATGTGGATCAGAGGTTAACTCTTTAGTGAGGAAATTCATCGTTTGGGTTCAAAA 245
21 AsnAlaaspGlyLysLeuSerVallyspPheGlyValLeuPheGlnAspAspArgCysAla 40
246 AATGCTGATGGAAGTTAAGCGTGAATTTGGGTCCTCTTCGCTGATGATAAATGTGCC 305
41 AsnLeuPheGluAlaLeuValGlyThrLeuLysAlaAlaLysArgArgLysIleValThr 60
306 AACCTCTTTGAAGCATTTGTAAGCACTTTAAAGCTGCAAAACGAAAGAGATTGTAAAC 365
61 TyrAlaGlyGluLeuLeuGlnGlyValHisAspValAspIleValLeuGln 80
366 TATCCAGGAGAGCTGCTTCTGCAAGGTTCATCATGATGATTTGACATTATATTACTGCAA 425
81 Asp 81
426 GAT 428

RESULT 9
US-10-373-556-3
; Sequence 3, Application US/10373556
; Publication No. US20030224402A1
; GENERAL INFORMATION:
; APPLICANT: Paul B. Fisher
; APPLICANT: Dong-chul Kang
; APPLICANT: Zao-Zhong Su
; TITLE OF INVENTION: PROGRESSION SUPPRESSED GENE 13 (PSGen13)
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: A34586-A-PCT-USA (070050.2305)
; CURRENT APPLICATION NUMBER: US/10/373,556
; CURRENT FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: PCT/US01/26795
; PRIOR FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: 09/648,310
; PRIOR FILING DATE: 2000-08-25
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 835
; TYPE: DNA
; ORGANISM: homo sapiens
; APPLICANT: Paul B. Fisher
; APPLICANT: Dong-chul Kang
; APPLICANT: Zao-Zhong Su
; TITLE OF INVENTION: PROGRESSION SUPPRESSED GENE 13 (PSGen13)
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: A34586-A-PCT-USA (070050.2305)
; CURRENT APPLICATION NUMBER: US/10/373,556
; CURRENT FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: PCT/US01/26795
; PRIOR FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: 09/648,310
; PRIOR FILING DATE: 2000-08-25
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 835
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-373-556-6

Alignment Scores:
Pred. No.: 1.78e-53 Length: 835
Score: 390.00 Matches: 76
Percent Similarity: 98.77% Conservative: 4
Best Local Similarity: 93.83% Mismatches: 1
Query Match: 96.06% Indels: 0
DB: 13 Gaps: 0

US-09-648-310-2 (1-81) x US-10-373-556-6 (1-835)
Qy 1 MetAsnValGluHisGluValAsnLeuValGluGluLeuHisArgLeuGlySerLys 20
Db 197 ATGAATGTGGATCAGAGGTTAACTCTTTAGTGAGGAAATTCATCGTTTGGGTTCAAAA 256
21 AsnAlaaspGlyLysLeuSerVallyspPheGlyValLeuPheGlnAspAspArgCysAla 40
Db 257 AATGCTGATGGAAGTTAAGCGTGAATTTGGGTCCTCTTCGCTGATGATAAATGTGCC 316
41 AsnLeuPheGluAlaLeuValGlyThrLeuLysAlaAlaLysArgArgLysIleValThr 60
Db 317 AACCTCTTTGAAGCATTTGTAAGCACTTTAAAGCTGCAAAACGAAAGAGATTGTAAAC 376
61 TyrAlaGlyGluLeuLeuGlnGlyValHisAspValAspIleValLeuGln 80
Db 377 TATCCAGGAGAGCTGCTTCTGCAAGGTTCATCATGATGATTTGACATTATATTACTGCAA 436
81 Asp 81
437 GAT 439

RESULT 11
US-10-342-887-156
; Sequence 156, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
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1 MetAsnValGluHisGluValAsnLeuValGluGluIleHisArgLeuGlySerLys 20

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Db 199 ATGAATGTGGATCAGGAGTTAACTTCTAGTGGAGGAAATTCATCGTTTGGTTCAAAA 258
Qy 21 AsnAlaaspGlyLysLeuSerValLysPheGlyValLeuPheGlnAspArgCysala 40
Db 259 AATGCTGATGGAAGTTACCGTGAATTTGGGGTCTCTTCGATGATATAATGTGCC 318
Qy 41 AsnLeuPheGlnAlaLeuValGlyThrLeuLysAlaAlaLysArgLysIleValThr 60
Db 319 AACCTCTTTGAAGCATTTGGTAGGAATCTTTAAAGCTGCAAAACGAAGGAGATTGTAACA 378
Qy 61 TyrAlaGlyLysLeuLeuGlnGlyValHisAspValAspIleValLeuLeuGln 80
Db 379 TATCCAGAGAGTGTCTTACAGGNGTTCATGATGATGTGACATTAATATTCTGCAA 438
Qy 81 Asp 81
Db 439 GAA 441

RESULT 14
US-09-969-034-748
; Sequence 748, Application US/09969034
; Publication No. US20040110668A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Astle, Jon H.
; APPLICANT: Carroll, Eddie III
; APPLICANT: Catino, Theodore J.
; APPLICANT: Deivedi, Poornima
; APPLICANT: Molino, Gary A.
; APPLICANT: Thiagalingam, Arunthathi
; APPLICANT: Lewis, Marcia E.
; TITLE OF INVENTION: Nucleic Acid Sequences Differentially
; TITLE OF INVENTION: Expressed in Cancer Tissue
; FILE REFERENCE: 1657/1032
; CURRENT APPLICATION NUMBER: US/09/969,034
; PRIOR FILING DATE: 2001-10-02
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 4494
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 748
; LENGTH: 717
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 452, 481, 482, 505, 521, 536, 540, 594, 599, 607, 635, 641,
; LOCATION: 643, 657, 664, 673, 691, 695, 700
; OTHER INFORMATION: n = A,T,C or G
US-09-969-034-748

Alignment Scores:
Pred. No.: 1.37e-52 Length: 717
Score: 384.00 Matches: 75
Percent Similarity: 98.75% Conservative: 4
Best Local Similarity: 93.75% Mismatches: 1
Query Match: 94.58% Indels: 0
DB: 12 Gaps: 0

US-09-648-310-2 (1-81) x US-09-969-034-748 (1-717)
Qy 1 MetAsnValGluHisGluValAsnLeuValGluGluLeuHisArgLeuGlySerLys 20
Db 202 ATGAATGTGGATCAGGAGTTAACTTCTAGTGGAGGAAATTCATCGTTTGGTTCAAAA 261
Qy 21 AsnAlaaspGlyLysLeuSerValLysPheGlyValLeuPheGlnAspArgCysala 40
Db 262 AATGCTGATGGAAGTTACCGTGAATTTGGGGTCTCTTCGATGATATAATGTGCC 321
Qy 41 AsnLeuPheGlnAlaLeuValGlyThrLeuLysAlaAlaLysArgLysIleValThr 60
Db 322 AACCTCTTTGAAGCATTTGGTAGGAATCTTTAAAGCTGCAAAACGAAGGAGATTGTAACA 381
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Qy 61 TyrAlaGlyLysLeuLeuGlnGlyValHisAspValAspIleValLeuLeuGln 80
Db 382 TATCCAGGAGAGTGTCTTCTACAGGTTGTTCTATGATGATTAATATTCTGCAA 441

RESULT 15
US-09-918-995-26075
; Sequence 26075, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hysseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26075
; LENGTH: 458
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(458)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-26075

Alignment Scores:
Pred. No.: 2.92e-50 Length: 458
Score: 368.00 Matches: 72
Percent Similarity: 98.68% Conservative: 3
Best Local Similarity: 94.74% Mismatches: 1
Query Match: 90.64% Indels: 0
DB: 10 Gaps: 0

US-09-648-310-2 (1-81) x US-09-918-995-26075 (1-458)
Qy 1 MetAsnValGluHisGluValAsnLeuValGluGluLeuHisArgLeuGlySerLys 20
Db 231 ATGAATGTGGATCAGGAGTTAACTTCTAGTGGAGGAAATTCATCGTTTGGTTCAAAA 290
Qy 21 AsnAlaaspGlyLysLeuSerValLysPheGlyValLeuPheGlnAspArgCysala 40
Db 291 AATGCTGATGGAAGTTAAAGCGTGAATTTGGGGTCTCTTCGATGATATAATGTGCC 350
Qy 41 AsnLeuPheGlnAlaLeuValGlyThrLeuLysAlaAlaLysArgLysIleValThr 60
Db 351 AACCTCTTTGAAGCATTTGGTAGGAATCTTTAAAGCTGCAAAACGAAGGAGATTGTAACA 410
Qy 61 TyrAlaGlyLysLeuLeuGlnGlyValHisAspValAspIleValLeuLeuGln 76
Db 411 TATCCAGGAGAGTGTCTTCTGCAAGGTTTCATGATGATGATGATGATGATGATGAT 458

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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 1, 2004, 20:15:24 ; Search time 61 Seconds
(without alignments)
736.902 Million cell updates/sec

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Perfect score: 410
Sequence: 1 MNVDHEVLLVEEHRIGSK.....PGELLOGVHDDVILLQD 81

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0
Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LOOPTXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFM=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09648310@cgn2_1_141_@runat_27082004_154406_27960 -NCPU=6 -ICPU=3
-NO MNAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA.*
1: /cgn2_6/ptdata/2/ina/5A.COMB.seq.*
2: /cgn2_6/ptdata/2/ina/5B.COMB.seq.*
3: /cgn2_6/ptdata/2/ina/6A.COMB.seq.*
4: /cgn2_6/ptdata/2/ina/6B.COMB.seq.*
5: /cgn2_6/ptdata/2/ina/PCTUS.COMB.seq.*
6: /cgn2_6/ptdata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	371	90.5	786	4	US-09-023-655-79 Sequence 79, Appl
2	352	85.9	800	4	US-09-644-460-26 Sequence 26, Appl
3	66	16.1	2133	4	US-09-328-352-1774 Sequence 1774, Ap
4	64.5	15.7	393	4	US-09-252-991A-12137 Sequence 12137, A
5	64.5	15.7	2323	1	US-08-358-901-1 Sequence 1, Appli
6	64.5	15.7	2323	1	US-08-566-347-1 Sequence 1, Appli
7	64.5	15.7	2323	1	US-08-693-835-1 Sequence 1, Appli
8	64	15.6	2329	1	US-08-457-797A-8 Sequence 8, Appli
9	64	15.6	2329	1	US-08-812-025-8 Sequence 8, Appli
10	64	15.6	2329	3	US-09-138-873A-8 Sequence 8, Appli
11	63	15.4	1278	4	US-09-134-000C-2571 Sequence 2571, Ap
12	63	15.4	14770	4	US-09-220-132-30 Sequence 30, Appl

c	13	62.5	15.2	675	4	US-09-252-991A-5194 Sequence 5194, Ap
c	14	62.5	15.2	954	4	US-09-252-991A-5307 Sequence 5307, Ap
c	15	62	15.1	1664976	4	US-08-916-421B-1 Sequence 1, Appli
c	16	61	14.9	885	4	US-09-328-352-1423 Sequence 1423, Ap
c	17	61	14.9	1074	1	US-08-008-216-3 Sequence 3, Appli
c	18	61	14.9	1074	1	US-08-459-569-3 Sequence 3, Appli
c	19	61	14.9	1074	1	US-08-458-831-3 Sequence 3, Appli
c	20	61	14.9	1385	4	US-09-107-532A-1659 Sequence 1659, Ap
c	21	61	14.9	6563	4	US-09-453-702B-192 Sequence 192, App
c	22	61	14.9	21126	1	US-08-008-216-19 Sequence 19, Appl
c	23	61	14.9	21126	1	US-08-459-569-19 Sequence 19, Appl
c	24	61	14.9	21126	1	US-08-458-831-19 Sequence 19, Appl
c	25	60.5	14.8	2082	4	US-09-107-532A-2158 Sequence 2158, Ap
c	26	60	14.6	582	4	US-09-252-991A-13907 Sequence 12907, A
c	27	60	14.6	1449	4	US-09-252-991A-13298 Sequence 13298, A
c	28	60	14.6	2028	4	US-09-252-991A-12977 Sequence 12977, A
c	29	60	14.6	2040	4	US-09-252-991A-12977 Sequence 12977, A
c	30	59.5	14.5	1134	4	US-09-252-991A-8104 Sequence 8104, Ap
c	31	59.5	14.5	1314	4	US-09-252-991A-8001 Sequence 8001, Ap
c	32	59.5	14.5	1755	4	US-09-252-991A-8133 Sequence 8133, Ap
c	33	59.5	14.5	3003	3	US-08-915-337-1 Sequence 1, Appli
c	34	59	14.4	1450	4	US-09-354-998A-1 Sequence 50, Appl
c	35	59	14.4	1740	4	US-08-851-567B-50 Sequence 7, Appli
c	36	59	14.4	3913	1	US-08-472-934-7 Sequence 7, Appli
c	37	59	14.4	3913	2	US-08-323-460A-7 Sequence 7, Appli
c	38	59	14.4	3913	3	US-08-461-146C-7 Sequence 7, Appli
c	39	59	14.4	3913	3	US-08-461-146C-7 Sequence 7, Appli
c	40	59	14.4	4592	1	US-08-628-829-11 Sequence 11, Appl
c	41	59	14.4	4592	1	US-08-472-934-9 Sequence 9, Appli
c	42	59	14.4	4592	2	US-08-323-460A-9 Sequence 9, Appli
c	43	59	14.4	4592	2	US-08-461-146C-9 Sequence 9, Appli
c	44	59	14.4	4592	3	US-08-461-146C-9 Sequence 9, Appli
c	45	59	14.4	5414	4	US-08-628-829-13 Sequence 13, Appl

ALIGNMENTS

RESULT 1

US-09-023-655-79
Sequence 79, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 855-0555
 TELEFAX: (650) 845-4166
 INFORMATION FOR SEQ ID NO: 79:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 786 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: THPLB01
 CLONE: 012364
 US-09-023-655-79

Alignment Scores:
 Pred. No.: 4,35e-50 Length: 786
 Score: 371.00 Matches: 81
 Percent Similarity: 96.43% Conservative: 0
 Best Local Similarity: 96.43% Mismatches: 0
 Query Match: 90.49% Indels: 3
 DB: 4 Gaps: 0

US-09-648-310-4 (1-81) x US-09-023-655-79 (1-786)

QY 1 MetAsnValAspHisGluValAsnLeuValGluGluHisArgLeuGlySerLys 20
 Db 140 ATCAATGTGGATCACGAGGTTAACTCTTAGTGGAGAAATTCATCGTTGGTTCAAAA 199
 QY 21 AsnAlaAspGlyLysLeuSerValLysPheGlyValLeuPheArgAspAspLysCysA 40
 Db 200 AATGCTGTGGAAGTTAAGCCGTGAATTTTGGGGTCTCTTCCGTGATGATAAATGTG 259
 QY 40 laAsnLeuPheGluAlaLeuValGlyThrLeuLysAlaAla-LysArgGlyLysileVal 59
 Db 260 CCAACTCTTTGAGGATTTGGTAGGACTCTTAAGCTGCAAAACGAGGAGATTGTA 319
 QY 60 ThrTyProGlyLeuLeuGlnGlyValHisAspValAspLysileleLeuLeu 79
 Db 320 ACATATCCAGGAGAGCTGCTTCTGCAAGGTGTTTCATGATGATGATGATGATGATGAT 379
 QY 80 GinAsp 81
 Db 380 CAGAT 385

RESULT 2

US-09-644-460-26
 ; Sequence 26, Application US/09644460
 ; Patent No. 6657053
 ; GENERAL INFORMATION:
 ; APPLICANT: Fisher, Paul B.
 ; TITLE OF INVENTION: Reciprocal Subtraction Differential
 ; FILE REFERENCE: Display
 ; CURRENT APPLICATION NUMBER: US/09/644,460
 ; PRIOR FILING DATE: 2000-08-23
 ; PRIOR APPLICATION NUMBER: PCT/US99/04323
 ; PRIOR FILING DATE: 1999-02-26
 ; PRIOR APPLICATION NUMBER: US 09/197,889
 ; PRIOR FILING DATE: 1998-11-23
 ; PRIOR APPLICATION NUMBER: US 09/185,115
 ; PRIOR FILING DATE: 1998-11-03
 ; PRIOR APPLICATION NUMBER: US 09/032,684
 ; PRIOR FILING DATE: 1998-02-27
 ; NUMBER OF SEQ ID NOS: 42
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 26
 ; LENGTH: 800
 ; TYPE: DNA
 ; ORGANISM: homo sapiens
 US-09-644-460-26

Alignment Scores:
 Pred. No.: 5.06e-47 Length: 800
 Score: 352.00 Matches: 74

Percent Similarity: 93.98% Conservative: 4
 Best Local Similarity: 89.16% Mismatches: 3
 Query Match: 85.85% Indels: 2
 DB: 4 Gaps: 0

US-09-648-310-4 (1-81) x US-09-644-460-26 (1-800)

QY 1 MetAsnValAspHisGluValAsnLeuValGluGluHisArgLeuGlySerLys 20
 Db 170 ATGAACGTGGAGCATGAGGTTAACTCTCTGTGGAGAAATTCATCGTCTGGGTCCAAA 229
 QY 21 AsnAlaAspGlyLysLeuSerValLysPheGlyValLeuPheArgAspAspLysCysAla 40
 Db 230 AATGCCGATGGAAACCTGAGTGTGAAGTTTGGGGTCTCTTCCAAGACGACAGATGTGCC 289
 QY 41 AsnLeuPheGluAla-LeuValGlyThrLeuLysAla-AlaLysArgGlyLysileVal 60
 Db 290 AATCTCTTTGAAACCGTTGGTGGGAACTCTGAAAGCCCGCAAAACGAAAGAGATTGTTA 349
 QY 60 hrTyProGlyGluLeuLeuGlnGlyValHisAspValAspLysileleLeuLeu 80
 Db 350 CGTACGCGAAGAGCTGCTTTTGCAGGTGTTTCATGATGATGATGATGATGATGATGAT 409
 QY 80 InAsp 81
 Db 410 AAGAT 414

RESULT 3

US-09-328-352-1774
 ; Sequence 1774, Application US/09328352
 ; Patent No. 6562958
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary L. Breton et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
 ; FILE REFERENCE: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
 ; CURRENT APPLICATION NUMBER: GTC99-03PA
 ; CURRENT FILING DATE: US/09/328,352
 ; NUMBER OF SEQ ID NOS: 1999-06-04
 ; SEQ ID NO 1774
 ; LENGTH: 2133
 ; TYPE: DNA
 ; ORGANISM: Acinetobacter baumannii
 US-09-328-352-1774

Alignment Scores:

Pred. No.: 1.95 Length: 2133
 Score: 66.00 Matches: 24
 Percent Similarity: 50.67% Conservative: 14
 Best Local Similarity: 32.00% Mismatches: 29
 Query Match: 16.10% Indels: 8
 DB: 4 Gaps: 4

US-09-648-310-4 (1-81) x US-09-328-352-1774 (1-2133)

QY 1 MetAsnValAspHisGluValAsnLeuValGluGluHisArgLeuGlySerLys 20
 Db 1396 ATGGTGTGACCGCTGAAACACAACTGCGTATGTTTCAT---TTAGAACGGGT 1452
 QY 21 Asn-----AlaAspGlyLysLeuSerValLysPheGlyValLeuPheArgAsp--- 36
 Db 1453 AACTACCATGCTATGATGCTCGCATTTATGATGATGATGATGATGATGATGATGATGATGAT 1512
 QY 37 AspLysCysAlaAsn-----LeuPheGluAlaLeuValGlyThrLeuLysAlaAla 53
 Db 1513 GACTTGTGACAGACGTACACCGCTATTTTCCAAGAGCTCACGGGTATGGTAAATGGCA 1572
 QY 54 LysArgArgLysileValThrTyProGlyGluLeuLeuGln 68
 Db 1573 AAAGTAAAGATTACTCCATGACCTTTTACTCTGCTGCTCAG 1617

RESULT 4

US-09-252-991A-12137

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; Sequence 12137, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 12137
; LENGTH: 393
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12137

Alignment Scores:
Pred. No.: 0.293 Length: 393
Score: 64.50 Matches: 21
Percent Similarity: 39.51% Conservative: 11
Best Local Similarity: 25.93% Mismatches: 38
Query Match: 15.73% Indels: 11
Ds: 4 Gaps: 2

US-09-648-310-4 (1-81) x US-09-252-991A-12137 (1-393)

QY 1 MetAsnValAspHisGluValAsnLeuLeuValGluHisArgLeuGlySerLys 20
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QY 21 AsnAlaAspGlyLysSerValLysPheGlyValLeuPheArgAspAspLysCysAla 40
Db 190 CGCGCGCATGGTCTCTTCGGCACGTCATAGCGGATGATCGAAGTGGCGAATCCGTCTC 249
QY 41 AsnLeuPheGluAlaLeuValGlyThrLeuLysAlaAlaLysArgArgLysIleValThr 60
Db 250 GACATCGCCCGCAGCTCGCGCGGTGGAAACGGCGGTACCGCGCAAGCGCTCGT 309
QY 61 TyrProGlyGluLeuLeuGlnGlyValHisAspValAspIleLeuLeuGln 80
Db 310 -----ATCCACGACCATCATCGACCATTTGCTGCCCAT 342
QY 81 Asp 81
Db 343 GAC 345

RESULT 5
US-08-358-901-1/c
; Sequence 1, Application US/08358901
; Patent No. 5554521
; GENERAL INFORMATION:
; APPLICANT: Suslow, Trevor V.
; APPLICANT: Jones, Jonathan D.G.
; TITLE OF INVENTION: No. 5554521el Chitinase-Producing Plants
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,901
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; FILING DATE: 19-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/550,253
; FILING DATE: 09-JUL-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/889,033
; FILING DATE: 18-JUL-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/593,691
; FILING DATE: 26-MAR-1984
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 12176-5-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2323 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 361..2043
US-08-358-901-1

Alignment Scores:
Pred. No.: 3.83 Length: 2323
Score: 64.50 Matches: 20
Percent Similarity: 52.94% Conservative: 16
Best Local Similarity: 29.41% Mismatches: 31
Query Match: 15.73% Indels: 1
Db: 1 Gaps: 1

US-09-648-310-4 (1-81) x US-08-358-901-1 (1-2323)

QY 5 HisGluValAsnLeuLeuValGluHisArgLeuGlySerLysAsnAlaAspGly 24
Db 1086 CACGCCCTCTCGCCCTTTTCAGCGCGCGGACGGATCGTGGATCGAGATTTTGA-- 1030
QY 25 LysLeuSerValLysPheGlyValLeuPheArgAspLysCysAlaAsnLeuPheGlu 44
Db 1029 GTCTCGCGCCTTGGCAGGAGCGCTCAACGCGCTGAAGCGCTTCAATCTCTTCAG 970
QY 45 AlaLeuValGlyThrLeuLysAlaAlaLysArgArgLysIleValThrTyrProGlyGlu 64
Db 969 GCTGTGTTGATGCGCTTGGCGCGCAGATCGGATTAAGCCGTACAGCAGGTGGTTCAG 910
QY 65 LeuLeuLeuGlnGlyValHisAsp 72
Db 909 GTTTTGGCGCGGATCTTGTGCAC 886

RESULT 6
US-08-566-347-1/c
; Sequence 1, Application US/08566347
; Patent No. 5633450
; GENERAL INFORMATION:
; APPLICANT: Suslow, Trevor V.
; APPLICANT: Jones, Jonathan D.G.
; TITLE OF INVENTION: No. 5633450el Chitinase-Producing Plants
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; APPLICATION NUMBER: US/08/566,347
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MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/566,347
 FILING DATE: 01-DEC-1995
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/358,901
 FILING DATE: 19-DEC-1994
 APPLICATION NUMBER: US 07/550,253
 FILING DATE: 09-JUL-1990
 APPLICATION NUMBER: US 06/888,033
 FILING DATE: 18-JUL-1986
 APPLICATION NUMBER: US 06/593,691
 FILING DATE: 26-MAR-1984
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith, William M.
 REGISTRATION NUMBER: 30,223
 REFERENCE/DOCKET NUMBER: 12176-5-3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-326-2400
 TELEFAX: 415-326-2422
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2323 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 361..2043
 US-08-566-347-1

Alignment Scores:
 Pred. No.: 3.83 Length: 2323
 Score: 64.50 Matches: 20
 Percent Similarity: 52.94% Conservative: 16
 Best Local Similarity: 29.41% Mismatches: 31
 Query Match: 15.73% Indels: 1
 DB: 1 Gaps: 1

US-09-648-310-4 (1-81) x US-08-566-347-1 (1-2323)

QY 5 HisGluValAsnLeuValGluGluLeHisArgLeuGlySerLysAsnAlaAspGly 24
 Db 1086 CAGCCCTTCTCGGCTTTTGACGCGCGGACGATCGTGATCGAGATTTTGA--- 1030
 QY 25 LysLeuSerValLysPheGlyValLeuPheArgAspLysCysAlaAsnLeuPheGlu 44
 Db 1029 GTCTCGCGGCTTGGCAGGCGCTGCAACGCTGGAAGCTGCTTCAATCTCTTCAG 970
 QY 45 AlaLeuValGlyThrLeuLysAlaAlaLysArgArgLysIleValThrTyrProGlyGlu 64
 Db 969 GCTGTCGTGTGATGCGATTCGCCCGCAGATCGGNTAAGCGTACACAGGTGGTTCAG 910
 QY 65 LeuLeuLeuGlnGlyValHisAsp 72
 Db 909 GTTTTGGCGGGATCTTGTGCAC 886

RESULT 7

US-08-693-835-1/c
 Sequence 1, Application US/08593835
 Patent No.: 5776448
 GENERAL INFORMATION:
 APPLICANT: Suslow, Trevor V.
 APPLICANT: Jones, Jonathan D.G.
 TITLE OF INVENTION: No. 5776448e1 Chitinase-Producing Plants

NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, 8th Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/693,835
 FILING DATE: 01-AUG-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/358,901
 FILING DATE: 19-DEC-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/550,253
 FILING DATE: 09-JUL-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 06/888,033
 FILING DATE: 18-JUL-1986
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 06/593,691
 FILING DATE: 26-MAR-1984
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith, William M.
 REGISTRATION NUMBER: 30,223
 REFERENCE/DOCKET NUMBER: 12176-5-3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-326-2400
 TELEFAX: 415-326-2422
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2323 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 361..2043
 US-08-693-835-1

Alignment Scores:
 Pred. No.: 3.83 Length: 2323
 Score: 64.50 Matches: 20
 Percent Similarity: 52.94% Conservative: 16
 Best Local Similarity: 29.41% Mismatches: 31
 Query Match: 15.73% Indels: 1
 DB: 1 Gaps: 1

US-09-648-310-4 (1-81) x US-08-693-835-1 (1-2323)

QY 5 HisGluValAsnLeuValGluGluLeHisArgLeuGlySerLysAsnAlaAspGly 24
 Db 1086 CAGCCCTTCTCGGCTTTTGACGCGCGGACGATCGTGATCGAGATTTTGA--- 1030
 QY 25 LysLeuSerValLysPheGlyValLeuPheArgAspLysCysAlaAsnLeuPheGlu 44
 Db 1029 GTCTCGCGGCTTGGCAGGCGCTGCAACGCTGGAAGCTGCTTCAATCTCTTCAG 970
 QY 45 AlaLeuValGlyThrLeuLysAlaAlaLysArgArgLysIleValThrTyrProGlyGlu 64
 Db 969 GCTGTCGTGTGATGCGATTCGCCCGCAGATCGGNTAAGCGTACACAGGTGGTTCAG 910
 QY 65 LeuLeuLeuGlnGlyValHisAsp 72
 Db 909 GTTTTGGCGGGATCTTGTGCAC 886

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RESULT 8
US-08-457-797A-8/c
; Sequence 8, Application US/08457797A
; Patent No. 5869045
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Transgenic pathogen-resistant organism
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brumbaugh, Graves, Donohue and Raymond
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,797A
; FILING DATE: June 1, 1995
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 18,839
; REFERENCE/DOCKET NUMBER: A29542 FWC - 37/31335
; TELEPHONE: (212) 408-2500
; TELEFAX: (212) 765-2519
; TELEX: 238555
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2329 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Serratia marcescens
; IMMEDIATE SOURCE:
; LIBRARY: Cosmid bank from Serratia marcescens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..2329
; IDENTIFICATION METHOD: experimental
; OTHER INFORMATION: /function= "exo-chitinase"
; OTHER INFORMATION: /product= "Chis protein"
; OTHER INFORMATION: /evidence= EXPERIMENTAL
; OTHER INFORMATION: /note= "sequence listing of the Chis gene from a
; US-08-457-797A-8
;
Alignment Scores:
Pred. No.: 4.63 Length: 2329
Score: 64.00 Matches: 17
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QY 46 LeuValGlyThrLeuLysAlaAlaLysArgArgLysIleValThrTyrProGlyGluLeu 65
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QY 66 LeuLeuGlnGlyValHisasp 72

RESULT 9
US-08-812-025-8/c
; Sequence 8, Application US/08812025
; Patent No. 5804184
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Transgenic pathogen-resistant organism
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brumbaugh, Graves, Donohue and Raymond
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/812,025
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Teiser, Arthur
; REGISTRATION NUMBER: 18,839
; NAME: Kole, Lisa
; REGISTRATION NUMBER: 35,225
; REFERENCE/DOCKET NUMBER: A29542 FWC - 37/31335
; TELEPHONE: (212) 408-2500
; TELEFAX: (212) 765-2519
; TELEX: 238555
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2329 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Serratia marcescens
; IMMEDIATE SOURCE:
; LIBRARY: Cosmid bank from Serratia marcescens
; FEATURE:
; NAME/KEY: misc feature
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QY 46 LeuValGlyThrLeuLysAlaAlaLysArgArgLysIleValThrTyrProGlyGluLeu 65
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Db 966 GTCTGTGATCCATTCGCCGCGAGATCGGATGATAAAGCCGTACAGCAGGTGGGTGAGGTT 907
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US-09-138-873A-8/c
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 ; Patent No. 6271438
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 ; APPLICANT:
 ; TITLE OF INVENTION: Transgenic pathogen-resistant organism
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Baker & Botts
 ; STREET: 30 Rockefeller Plaza
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10112
 ; COMPUTER READABLE FORM:
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 ; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/138,873A
 ; FILING DATE: August 24, 1998
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Tensey, Arthur
 ; REGISTRATION NUMBER: 18,839
 ; NAME: Kole, Lisa
 ; REGISTRATION NUMBER: 35,225
 ; REFERENCE/DOCKET NUMBER: A29542 FWC - 37/31335
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 408-2500
 ; TELEFAX: (212) 765-2519
 ; TELEX: 238555
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2329 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; ORIGINAL SOURCE:
 ; ORGANISM: Serratia marcescens
 ; IMMEDIATE SOURCE:
 ; LIBRARY: Cosmid bank from Serratia marcescens
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US-09-648-310-4 (1-81) x US-09-138-873A-8 (1-2329)

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RESULT 11

US-09-134-000C-2571
 ; Sequence 2571, Application US/09134000C
 ; Patent No. 6617156
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn Doucette-Stamm et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
 ; ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 032796-032
 ; CURRENT APPLICATION NUMBER: US/09/134,000C
 ; PRIOR FILING DATE: 1998-08-13
 ; PRIOR APPLICATION NUMBER: US 60/055,778
 ; PRIOR FILING DATE: 1997-08-15
 ; NUMBER OF SEQ ID NOS: 6812
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 2571
 ; LENGTH: 1278
 ; TYPE: DNA
 ; ORGANISM: Enterococcus faecalis
 ; US-09-134-000C-2571

Alignment Scores:

Pred. No.: 2.81 Length: 1278
 Score: 63.00 Matches: 21
 Percent Similarity: 38.46% Conservative: 14
 Best Local Similarity: 23.08% Mismatches: 28
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US-09-648-310-4 (1-81) x US-09-134-000C-2571 (1-1278)

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Qy 21 AsnAlaAspGlyLysLeuSerVal----- 28

Db 115 CTGTCAGGAGGATGACAGCTTACTTTATACAGATTCTGTTGGTCAGCAACAAAGTAT 174

Qy 29 -----LysPheGlyValLeuPheArgAspLysCysAlaAsnLeu 42

Db 175 GTGCAAGCCAAACTGAGGCGTTTGACTGGAAACGCAATTGACGAGTCGGGATCTG 234

Qy 43 PheGluAlaLeuValGlyThrLeuLysAlaAlaLysArgLysIleValThrTyrPro 62

Db 235 TTTTGTGAGTGCAGGAACG-----GAATTTCCT 264

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RESULT 12

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 ; Patent No. 6506607
 ; GENERAL INFORMATION:
 ; APPLICANT: Shyjan, Andrew W.
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE IDENTIFICATION AND ASSESSMENT
 ; OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCER
 ; FILE REFERENCE: 07334-074001
 ; CURRENT APPLICATION NUMBER: US/09/220,132
 ; CURRENT FILING DATE: 1998-12-23

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; Patent No. 6503729
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; APPLICANT: Buit et al.
; TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococcus
; Patent No. 6503729
; FILE OF INVENTION: jannaschii
; FILE REFERENCE: PB275
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; PRIOR FILING DATE: 1996-08-22
; NUMBER OF SEQ ID NOS: 3
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US-08-916-421B-1

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US-09-648-310-4 (1-81) x US-08-916-421B-1 (1-1664976)

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

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Perfect score: 410

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SUMMARIES

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4	410	100.0	483	16	US-10-242-535A-56189	Sequence 56189, A
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6	410	100.0	778	9	US-09-925-300-545	Sequence 545, App
7	410	100.0	835	13	US-10-373-556-3	Sequence 3, Appli
8	410	100.0	835	13	US-10-373-556-6	Sequence 6, Appli
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10	410	100.0	876	13	US-10-172-118-156	Sequence 156, App
11	406	99.0	594	12	US-09-969-034-750	Sequence 750, App
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16	371	90.5	786	17	US-10-641-643-79	Sequence 79, Appl
17	352	85.9	800	17	US-10-725-969A-26	Sequence 26, Appl
18	295	72.0	533	13	US-10-425-114-19867	Sequence 19867, A
19	286	69.8	486	9	US-09-938-842A-355	Sequence 355, App
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22	276	67.3	818	17	US-10-437-963-43648	Sequence 43648, A
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24	252	61.5	552	9	US-09-920-300A-939	Sequence 939, App
25	252	61.5	552	14	US-10-033-528-939	Sequence 939, App
26	252	61.5	552	15	US-10-099-926-939	Sequence 939, App
27	231	56.3	268	9	US-09-294-093B-2020	Sequence 2020, Ap
28	216	52.7	388	9	US-09-925-299-318	Sequence 318, App
29	216	52.7	388	10	US-09-925-299-318	Sequence 318, App
30	149	36.3	289	9	US-09-294-093B-4150	Sequence 4150, Ap
31	108	26.3	388	16	US-10-191-803-820	Sequence 820, App
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38	80.5	19.6	2960	17	US-10-437-963-34365	Sequence 34365, A
39	72.5	17.7	1359	17	US-10-437-963-82252	Sequence 82252, A
40	71.5	17.4	1107	13	US-10-425-114-33343	Sequence 33343, A
41	71.5	17.4	2163	13	US-10-425-114-30828	Sequence 30828, A
42	70	17.1	1728	13	US-10-282-122A-16022	Sequence 16022, A
43	68	16.6	2232	17	US-10-437-963-53833	Sequence 53833, A
44	67	16.3	2062	13	US-10-424-599-142059	Sequence 142059, A
45	66	16.1	553	17	US-10-437-963-92788	Sequence 92788, A

ALIGNMENTS

RESULT 1

US-10-085-783A-21733
; Sequence 21733, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Lieuw, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085.783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21733
; LENGTH: 400
; TYPE: DNA
; ORGANISM: Human

```
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (23)-(23)
/ OTHER INFORMATION: n is a, c, g, or t
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (48)-(48)
/ OTHER INFORMATION: n is a, c, g, or t
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (328)-(328)
/ OTHER INFORMATION: n is a, c, g, or t
US-10-085-783A-21733
```

```
Alignment Scores:
Pred. No.: 1.95e-58 Length: 400
Score: 410.00 Matches: 81
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0
```

US-09-648-310-4 (1-81) x US-10-085-783A-21733 (1-400)

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QY 1 MetAsnValAspHisGluValAsnLeuValGluLeuHisArgLeuGlySerLys 20
DB 77 ATGAATGTGGATCACCAGGTTAACTCTTAGTGGAGAAATTCATCGTTGGGTTCAAAA 136
QY 21 AsnAlaAspGlyLysLeuSerValLysPheGlyValLeuPheArgAspLysCysAla 40
DB 137 AATGCTGTGAAGTTAAGCGTGAATTTGGGTCCTCTTCGTCATGATAAATGTGCC 196
QY 41 AsnLeuPheGluAlaLeuValGlyThrLeuLysAlaAlaLysArgGlyLysValThr 60
DB 197 AACCTCTTTGAAGCATTTGGTAGGAATCTTAAGCTGCAAAACGAAGGAAGATTGTAACA 256
QY 61 TyrProGlyLysLeuLeuGlyValHisAspValAspLysLeuLeuGlyLys 80
DB 257 TATCCAGGAGAGCTGCTTCTGCAAGGTTCATGATGATGATGATGATGATGATGATGCA 316
QY 81 Asp 81
DB 317 GAT 319
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RESULT 2

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US-10-242-535A-21733
/ Sequence 21733, Application US/10242535A
/ Publication No. US20040013663A1
/ GENERAL INFORMATION:
/ APPLICANT: ChondroGene Inc.
/ APPLICANT: Liew, C.C.
/ TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
/ FILE REFERENCE: 4231/2005
/ CURRENT FILING DATE: 2002-09-12
/ PRIOR APPLICATION NUMBER: US 10/085,783
/ PRIOR FILING DATE: 2002-02-28
/ PRIOR APPLICATION NUMBER: US 60/305,340
/ PRIOR FILING DATE: 2001-07-13
/ PRIOR APPLICATION NUMBER: US 60/275,017
/ PRIOR FILING DATE: 2001-03-12
/ PRIOR APPLICATION NUMBER: US 60/271,955
/ PRIOR FILING DATE: 2001-02-28
/ NUMBER OF SEQ ID NOS: 58994
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 21733
/ LENGTH: 400
/ TYPE: DNA
/ ORGANISM: Human
```

```
FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (23)-(23)
/ OTHER INFORMATION: n is a, c, g, or t
```

```
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (48)-(48)
/ OTHER INFORMATION: n is a, c, g, or t
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (328)-(328)
/ OTHER INFORMATION: n is a, c, g, or t
US-10-242-535A-21733
```

```
Alignment Scores:
Pred. No.: 1.95e-58 Length: 400
Score: 410.00 Matches: 81
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 16 Gaps: 0
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US-09-648-310-4 (1-81) x US-10-242-535A-21733 (1-400)

```
QY 1 MetAsnValAspHisGluValAsnLeuValGluLeuHisArgLeuGlySerLys 20
DB 77 ATGAATGTGGATCACCAGGTTAACTCTTAGTGGAGAAATTCATCGTTGGGTTCAAAA 136
QY 21 AsnAlaAspGlyLysLeuSerValLysPheGlyValLeuPheArgAspLysCysAla 40
DB 137 AATGCTGTGAAGTTAAGCGTGAATTTGGGTCCTCTTCGTCATGATAAATGTGCC 196
QY 41 AsnLeuPheGluAlaLeuValGlyThrLeuLysAlaAlaLysArgGlyLysValThr 60
DB 197 AACCTCTTTGAAGCATTTGGTAGGAATCTTAAGCTGCAAAACGAAGGAAGATTGTAACA 256
QY 61 TyrProGlyLysLeuLeuGlyValHisAspValAspLysLeuLeuGlyLys 80
DB 257 TATCCAGGAGAGCTGCTTCTGCAAGGTTCATGATGATGATGATGATGATGATGCA 316
QY 81 Asp 81
DB 317 GAT 319
```

RESULT 3

```
US-10-085-783A-56189
/ Sequence 56189, Application US/10085783A
/ Publication No. US20040037841A1
/ GENERAL INFORMATION:
/ APPLICANT: ChondroGene Inc.
/ APPLICANT: Liew, C.C.
/ TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
/ FILE REFERENCE: 4231/2002
/ CURRENT FILING DATE: 2002-02-28
/ PRIOR APPLICATION NUMBER: US/10/085,783A
/ PRIOR FILING DATE: 2001-07-13
/ PRIOR APPLICATION NUMBER: US 60/305,340
/ PRIOR FILING DATE: 2001-03-12
/ PRIOR APPLICATION NUMBER: US 60/275,017
/ PRIOR FILING DATE: 2001-02-28
/ PRIOR APPLICATION NUMBER: US 60/271,955
/ PRIOR FILING DATE: 2001-02-28
/ NUMBER OF SEQ ID NOS: 58994
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 56189
/ LENGTH: 483
/ TYPE: DNA
/ ORGANISM: Human
```

US-10-085-783A-56189

```
Alignment Scores:
Pred. No.: 2.59e-58 Length: 483
Score: 410.00 Matches: 81
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0
```

261 TATCCAGGAGAGCTGCTTCTGCAAGGTGTTCATGATGTTGACATTATATTA

Qy 81 Asp 81
|||
Db 321 GAT 323

```

RESULT 5
US-09-969-034-557/c
; Sequence 557, Application US/09969034
; Publication NO. US20040110668A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Astle, Jon H.
; APPLICANT: Carroll, Eddie III
; APPLICANT: Catino, Theodore J.
; APPLICANT: Dwivedi, Poornima
; APPLICANT: Molino, Gary A.
; APPLICANT: Thiagalingam, Arunthathi
; APPLICANT: Lewis, Marcia E.
; TITLE OF INVENTION: Nucleic Acid Sequences Differentially
; TITLE OF INVENTION: Expressed in Cancer Tissue
; FILE REFERENCE: 1657/1032
; CURRENT APPLICATION NUMBER: US/09/969,034
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/237,271
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 4494
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 557
; LENGTH: 627
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 503, 512, 539, 596, 620
; OTHER INFORMATION: n = A,T,C or G
US-09-969-034-557

```

Alignment Scores:		
Pred. No.:	3,828-58	Length: 627
Score:	410.00	Matches: 81
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	100.00%	Indels: 0
DB:	12	Gaps: 0
US-09-648-310-4 (1-81)	x	US-09-969-034-557 (1-627)

Qy		1	MetAsnValAspHisGluValAsnLeuLeuValGluGlutIleHisArgLeuLeuGlySerIys	20
Db		271	ATCAATGTGGATTACCGAGGTTAAACCTCTTACTGAGGAATAATCATCTGTTGGGTTCAAAA	212
Qy		21	AnaAlaAspGlyLysLeuSerVailysPheGlyValLeuPheArgAspAspLysCysAla	40
Db		211	NATGCTGATGGAACCTTAAGCGTGAAATTTGGGGTCCCTCTCCGTGATGATAAATGTGCC	15
Qy		41	AsnLeuPheGluAlaLeuValGlyThrLeuLysAlaAlaLysArgArgLysIleValThr	60
Db		151	AACCTCTTTGAAGCATTTGGTAGGACTCTTAAAGCTGCAACAAGAAGAAATTTGTAACA	92
Qy		61	TyrProGlyGluLeuLeuGlnGlyValHisAspValAspIleIleLeuLeuGln	80
Db		91	TATCCNAGGAGCTGCTCTCSAAGGTGTTTCATGATGATGTTGACATTAATTAATTACTCAA	32
Qy		81	Asp	81
Db		31	GAT	29

RESULT 6
US-09-925-300-545
; Sequence 545, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:

; APPLICANT: Craig Rosen,
 ; APPLICANT: Steve Ruben
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 ; FILE REFERENCE: FA101
 ; CURRENT APPLICATION NUMBER: US/09/925,300
 ; PRIOR FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: PCT/US00/05988
 ; PRIOR FILING DATE: 2000-03-08
 ; PRIOR APPLICATION NUMBER: 60/124,270
 ; PRIOR FILING DATE: 1999-03-12
 ; NUMBER OF SEQ ID NOS: 1890
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 545
 ; LENGTH: 778
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (641)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; NAME/KEY: misc feature
 ; LOCATION: (652)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; US-09-925-300-545

Alignment Scores:
 Pred. No.: 5,28e-58 Length: 778
 Score: 410.00 Matches: 81
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-09-648-310-4 (1-81) x US-09-925-300-545 (1-778)

QY 1 MetAsnValAspHisGluValAsnLeuValGluLeuHisArgLeuGlySerLys 20
 Db 186 ATGAATGTCGATCAGAGTTAACTCTTAGTGGAGAAATTCATCGTTGGGTTCAAAA 245
 QY 21 AsnAlaAspGlyLysLeuSerValLysPheGlyValLeuPheArgAspLysCysAla 40
 Db 246 AATGCTGATGGAAGTTAAGCGTGAATTTGGGGTCTCTCCGTGATGATAAATGTGCC 305
 QY 41 AsnLeuPheGluAlaLeuValGlyThrLeuLysAlaAlaLysArgLysIleValThr 60
 Db 306 AACCTCTTTGAAGCATGTGTAGAACTCTTAAGCTGCAAAACGAGGAAGATTGTAA 365
 QY 61 TyrProGlyGluLeuLeuGlnGlyValHisAspValAspIleLeuLeuGln 80
 Db 366 TATCCAGGAGAGTGTCTTCTGCAAGGTGTTCATGATGATGATTATATTACTGCAA 425
 QY 81 Asp 81
 Db 426 GAT 428

RESULT 7
 US-10-373-556-3
 ; Sequence 3, Application US/10373556
 ; Publication No. US20030224402A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Paul B. Fisher
 ; APPLICANT: Dong-chul Kang
 ; APPLICANT: Zao-Zhong Su
 ; TITLE OF INVENTION: PROGRESSION SUPPRESSED GENE 13 (PSGen13)
 ; FILE REFERENCE: A34586-A-PCT-USA (070050.2305)
 ; CURRENT APPLICATION NUMBER: US/10/373,556
 ; PRIOR FILING DATE: 2003-02-24
 ; PRIOR APPLICATION NUMBER: PCT/US01/26795
 ; PRIOR FILING DATE: 2001-08-27
 ; PRIOR APPLICATION NUMBER: 09/648,310
 ; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 835
 ; TYPE: DNA
 ; ORGANISM: homo sapiens
 ; US-10-373-556-3

Alignment Scores:
 Pred. No.: 5,86e-58 Length: 835
 Score: 410.00 Matches: 81
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 13 Gaps: 0

US-09-648-310-4 (1-81) x US-10-373-556-3 (1-835)

QY 1 MetAsnValAspHisGluValAsnLeuValGluLeuHisArgLeuGlySerLys 20
 Db 197 ATGAATGTCGATCAGAGTTAACTCTTAGTGGAGAAATTCATCGTTGGGTTCAAAA 256
 QY 21 AsnAlaAspGlyLysLeuSerValLysPheGlyValLeuPheArgAspLysCysAla 40
 Db 257 AATGCTGATGGAAGTTAAGCGTGAATTTGGGGTCTCTCTCCGTGATGATAAATGTGCC 316
 QY 41 AsnLeuPheGluAlaLeuValGlyThrLeuLysAlaAlaLysArgLysIleValThr 60
 Db 317 AACCTCTTTGAAGCATGTGTAGAACTCTTAAGCTGCAAAACGAGGAAGATTGTAA 376
 QY 61 TyrProGlyGluLeuLeuGlnGlyValHisAspValAspIleLeuLeuGln 80
 Db 377 TATCCAGGAGAGTGTCTTCTGCAAGGTGTTCATGATGATGATTATATTACTGCAA 436
 QY 81 Asp 81
 Db 437 GAT 439

RESULT 8
 US-10-373-556-6
 ; Sequence 6, Application US/10373556
 ; Publication No. US20030224402A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Paul B. Fisher
 ; APPLICANT: Dong-chul Kang
 ; APPLICANT: Zao-Zhong Su
 ; TITLE OF INVENTION: PROGRESSION SUPPRESSED GENE 13 (PSGen13)
 ; FILE REFERENCE: A34586-A-PCT-USA (070050.2305)
 ; CURRENT APPLICATION NUMBER: US/10/373,556
 ; PRIOR FILING DATE: 2003-02-24
 ; PRIOR APPLICATION NUMBER: PCT/US01/26795
 ; PRIOR FILING DATE: 2001-08-27
 ; PRIOR APPLICATION NUMBER: 09/648,310
 ; PRIOR FILING DATE: 2000-08-25
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 6
 ; LENGTH: 835
 ; TYPE: DNA
 ; ORGANISM: homo sapiens
 ; US-10-373-556-6

Alignment Scores:
 Pred. No.: 5,86e-58 Length: 835
 Score: 410.00 Matches: 81
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 13 Gaps: 0

US-09-648-310-4 (1-81) x US-10-373-556-6 (1-835)

QY 1 MetAsnValAspHisGluValAsnLeuValGluLeuHisArgLeuGlySerLys 20

```

Db 197 ATGAATGTGGATCAGAGGTTAACTCTTAGTGGAGAAATTCATCGTTTGGGTCAAAA 256
Qy 21 AsnAlaAspGlyLysLeuSerValLysPheGlyValLeuPheArgAspAspLysCysAla 40
Db 257 AATGCTGATGGAAGTTAAGCGTGAATTTGGGGTCTCTTCCTCGATGATAAATGTGCC 316
Qy 41 AsnLeuPheGluAlaLeuValGlyThrLeuLysAlaLysArgLysIleValThr 60
Db 317 AACCTCTTTGAAGCATTTGGTAGAACTCTTAAAGCTGCAAAACGAAGAGATTGTAACA 376
Qy 61 TyrProGlyGluLeuLeuGlnGlyValHisAspValAspIleLeuLeuGln 80
Db 377 TATCCAGAGAGCTGCTTCTGCAAGGTGTTTCATGATGATGTGACATTATATTACTGCAA 436
Qy 81 Asp 81
Db 437 GAT 439

```

RESULT 9

```

US-10-342-887-156
; Sequence 156, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 156
; LENGTH: 876
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-156

```

```

Alignment Scores:
Pred. No.: 6,3e-58 Length: 876
Score: 410.00 Matches: 81
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

```

```

US-09-648-310-4 (1-81) x US-10-342-887-156 (1-876)
Qy 1 MetAsnValAspHisGluValAsnLeuValGluGluIleHisArgLeuGlySerLys 20
Db 136 ATGAATGTGGATCAGAGGTTAACTCTTAGTGGAGAAATTCATCGTTTGGGTCAAAA 195
Qy 21 AsnAlaAspGlyLysLeuSerValLysPheGlyValLeuPheArgAspAspLysCysAla 40
Db 196 AATGCTGATGGAAGTTAAGCGTGAATTTGGGGTCTCTTCCTCGATGATAAATGTGCC 255
Qy 41 AsnLeuPheGluAlaLeuValGlyThrLeuLysAlaLysArgLysIleValThr 60
Db 256 AACCTCTTTGAAGCATTTGGTAGAACTCTTAAAGCTGCAAAACGAAGAGATTGTAACA 315
Qy 61 TyrProGlyGluLeuLeuGlnGlyValHisAspValAspIleLeuLeuGln 80

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```

Db 316 TATCCAGGAGAGCTGCTTCTGCAAGGTGTTTCATGATGATGTGACATTATATTACTGCAA 375
Qy 81 Asp 81
Db 376 GAT 378
RESULT 10
US-10-172-118-156
; Sequence 156, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 156
; LENGTH: 876
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AF116682
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-156

```

```

Alignment Scores:
Pred. No.: 6,3e-58 Length: 876
Score: 410.00 Matches: 81
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

```

```

US-09-648-310-4 (1-81) x US-10-172-118-156 (1-876)
Qy 1 MetAsnValAspHisGluValAsnLeuValGluGluIleHisArgLeuGlySerLys 20
Db 136 ATGAATGTGGATCAGAGGTTAACTCTTAGTGGAGAAATTCATCGTTTGGGTCAAAA 195
Qy 21 AsnAlaAspGlyLysLeuSerValLysPheGlyValLeuPheArgAspAspLysCysAla 40
Db 196 AATGCTGATGGAAGTTAAGCGTGAATTTGGGGTCTCTTCCTCGATGATAAATGTGCC 255
Qy 41 AsnLeuPheGluAlaLeuValGlyThrLeuLysAlaLysArgLysIleValThr 60
Db 256 AACCTCTTTGAAGCATTTGGTAGAACTCTTAAAGCTGCAAAACGAAGAGATTGTAACA 315
Qy 61 TyrProGlyGluLeuLeuGlnGlyValHisAspValAspIleLeuLeuGln 80
Db 316 TATCCAGGAGAGCTGCTTCTGCAAGGTGTTTCATGATGATGTGACATTATATTACTGCAA 375
Qy 81 Asp 81
Db 376 GAT 378

```

RESULT 11

```

US-09-648-310-4 (1-81) x US-10-172-118-156 (1-876)
; Sequence 156, Application US/09969034
; Publication No. US20040110668A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Astle, Jon H.
; APPLICANT: Carroll, Eddie III

```

```

; APPLICANT: Catino, Theodore J.
; APPLICANT: Dwivedi, Poorima
; APPLICANT: Molino, Gary A.
; APPLICANT: Thiagalingam, Arunthathi
; APPLICANT: Lewis, Marcia E.
; TITLE OF INVENTION: Nucleic Acid Sequences Differentially
; FILE REFERENCE: 1657/1032
; CURRENT APPLICATION NUMBER: US/09/969,034
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/237,271
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 4494
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 750
; LENGTH: 594
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 405, 447, 472, 485, 497, 513, 534, 537, 541, 543, 563, 572
; OTHER INFORMATION: n = A,T,C or G
US-09-969-034-750

Alignment Scores:
Pred. No.: 1,64e-57 Length: 594
Score: 406.00 Matches: 80
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 98.77% Mismatches: 0
Query Match: 99.02% Indels: 0
DB: 12 Gaps: 0

US-09-648-310-4 (1-81) x US-09-969-034-750 (1-594)
QY 1 MetAsnValAspHisGluValAsnLeuValGluGluHisArgLeuGlySerLys 20
Db 199 ATGAATGTGGATCAGGAGTTAACTCTTAGTGGAGAAATTCATCGTTGGGTTCAAAA 258
QY 21 AsnAlaAspGlyValSerValLysPheGlyValLeuPheArgAspLysCysAla 40
Db 259 AATGCTGTGGTAAAGTTAAGCGTGAATTTGGGGTCTCTCCGTGATGATAATGTGCC 318
QY 41 AsnLeuPheGluAlaLeuValGlyThrLeuLysAlaAlaLysArgArgLysValThr 60
Db 319 AACCTCTTTGAAGCAATGTGTAGAACTCTTAAAGCTGCAAAACGAAGAGATTGTAACA 378
QY 61 TyrProGlyGluLeuLeuGlnGlyValHisAspAspValAspLysLeuLeuGln 80
Db 379 TATCCAGGAGAGCTGCTTCTCAAGGNGTTCAATGATGATTTGACATTATATTACTGCAA 438
QY 81 Asp 81
Db 439 GAA 441

RESULT 12
US-09-969-034-748
; Sequence 748, Application US/09969034
; Publication No. US20040110668A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Astle, Jon H.
; APPLICANT: Carroll, Eddie III
; APPLICANT: Catino, Theodore J.
; APPLICANT: Dwivedi, Poorima
; APPLICANT: Molino, Gary A.
; APPLICANT: Thiagalingam, Arunthathi
; APPLICANT: Lewis, Marcia E.
; TITLE OF INVENTION: Nucleic Acid Sequences Differentially
; FILE REFERENCE: 1657/1032
; CURRENT APPLICATION NUMBER: US/09/969,034
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/237,271

```

```

; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 4494
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 748
; LENGTH: 717
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 452, 481, 482, 505, 521, 536, 540, 594, 599, 607, 635, 641,
; LOCATION: 643, 657, 664, 673, 691, 695, 700
; OTHER INFORMATION: n = A,T,C or G
US-09-969-034-748

Alignment Scores:
Pred. No.: 4,68e-57 Length: 717
Score: 404.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.54% Indels: 0
DB: 12 Gaps: 0

US-09-648-310-4 (1-81) x US-09-969-034-748 (1-717)
QY 1 MetAsnValAspHisGluValAsnLeuValGluGluHisArgLeuGlySerLys 20
Db 202 ATGAATGTGGATCAGGAGTTAACTCTTAGTGGAGAAATTCATCGTTGGGTTCAAAA 261
QY 21 AsnAlaAspGlyValSerValLysPheGlyValLeuPheArgAspLysCysAla 40
Db 262 AATGCTGTGGTAAAGTTAAGCGTGAATTTGGGGTCTCTCCGTGATGATAATGTGCC 321
QY 41 AsnLeuPheGluAlaLeuValGlyThrLeuLysAlaAlaLysArgArgLysValThr 60
Db 322 AACCTCTTTGAAGCAATGTGTAGAACTCTTAAAGCTGCAAAACGAAGAGATTGTAACA 381
QY 61 TyrProGlyGluLeuLeuGlnGlyValHisAspAspValAspLysLeuLeuGln 80
Db 382 TATCCAGGAGAGCTGCTTCTCAAGGTTTCAATGATGATTTGACATTATATTACTGCAA 441

RESULT 13
US-10-373-556-1
; Sequence 1, Application US/10373556
; Publication No. US20030224402A1
; GENERAL INFORMATION:
; APPLICANT: Paul B. Fisher
; APPLICANT: Dong-chul Kang
; APPLICANT: Zhao-Zhong Su
; TITLE OF INVENTION: PROGRESSION SUPPRESSED GENE 13 (PSGen13)
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: A34586-A-PCT-USA (070050.2305)
; CURRENT APPLICATION NUMBER: US/10/373,556
; PRIOR FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: PCT/US01/26795
; PRIOR FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: 09/648,310
; PRIOR FILING DATE: 2000-08-25
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 780
; TYPE: DNA
; ORGANISM: rattus norvegicus
US-10-373-556-1

Alignment Scores:
Pred. No.: 1,15e-54 Length: 780
Score: 390.00 Matches: 76
Percent Similarity: 98.77% Conservative: 4
Best Local Similarity: 93.83% Mismatches: 1
Query Match: 95.12% Indels: 0
DB: 13 Gaps: 0

```


US-09-648-310-4 (1-81) x US-10-373-556-1 (1-780)

```
QY      1 MetAsnValAspHisGluValAsnLeuValGluGluHisArgLeuGlySerLys 20
      |||
Db      170 ATGACGTGGAGCATGAGGTTAACTCTGCTGGTGAGGAAATTCATCGTCTGGGTTCCAAA 229
      |||
QY      21 AsnAlaAspGlyLysLeuSerValLysPheGlyValLeuPheArgAspAspLysCysAla 40
      |||
Db      230 AATGCCGATGGGAAACTGAGTGTGAAGTTTGGGGTCTCTTCCAAAGACGACAGATGTGCC 289
      |||
QY      41 AsnLeuPheGluAlaLeuValGlyThrLeuLysAlaAlaLysArgArgLysIleValThr 60
      |||
Db      290 AATCTCTTTGACGCTTGGTGGAACTCTGAAGCGCGCAAAACGAGGAGATGTTAGC 349
      |||
QY      61 TyrProGlyGluLeuLeuGlnGlyValHisAspValAspValAspLleLeuLeuGln 80
      |||
Db      350 TACGCAGGAGAGCTGCTTTTGAAGGTGTTTCATGATGATGTTGACATTTGATTGTGCAA 409
      |||
QY      81 Asp 81
      |||
Db      410 GAT 412
```

RESULT 14

US-10-373-556-5

; Sequence 5, Application US/10373556

; Publication No. US20030224402A1

; GENERAL INFORMATION:

; APPLICANT: Paul B. Fisher

; APPLICANT: Dong-chul Kang

; APPLICANT: Zao-Zhong Su

; TITLE OF INVENTION: PROGRESSION SUPPRESSED GENE 13 (PSGen13)

; TITLE OF INVENTION: AND USES THEREOF

; FILE REFERENCE: A34586-A-PCT-USA (070050,2305)

; CURRENT APPLICATION NUMBER: US/10/373,556

; PRIOR FILING DATE: 2003-02-24

; PRIOR APPLICATION NUMBER: PCT/US01/26795

; PRIOR FILING DATE: 2001-08-27

; PRIOR APPLICATION NUMBER: 09/648,310

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 5

; TYPE: DNA

; ORGANISM: rattus norvegicus

US-10-373-556-5

Alignment Scores:

```
Pred. No.:      1.15e-54      Length:      780
Score:          390.00      Matches:      76
Percent Similarity: 98.77%      Conservative: 4
Best Local Similarity: 93.83%      Mismatches:  1
Query Match:     95.12%      Indels:      0
DB:              13          Gaps:         0
```

US-09-648-310-4 (1-81) x US-10-373-556-5 (1-780)

```
QY      1 MetAsnValAspHisGluValAsnLeuValGluGluHisArgLeuGlySerLys 20
      |||
Db      170 ATGACGTGGAGCATGAGGTTAACTCTGCTGGTGAGGAAATTCATCGTCTGGGTTCCAAA 229
      |||
QY      21 AsnAlaAspGlyLysLeuSerValLysPheGlyValLeuPheArgAspAspLysCysAla 40
      |||
Db      230 AATGCCGATGGGAAACTGAGTGTGAAGTTTGGGGTCTCTTCCAAAGACGACAGATGTGCC 289
      |||
QY      41 AsnLeuPheGluAlaLeuValGlyThrLeuLysAlaAlaLysArgArgLysIleValThr 60
      |||
Db      290 AATCTCTTTGACGCTTGGTGGAACTCTGAAGCGCGCAAAACGAGGAGATGTTAGC 349
      |||
QY      61 TyrProGlyGluLeuLeuGlnGlyValHisAspValAspValAspLleLeuLeuGln 80
      |||
Db      350 TACGCAGGAGAGCTGCTTTTGAAGGTGTTTCATGATGATGTTGACATTTGATTGTGCAA 409
      |||
```

Search completed: September 2, 2004, 00:02:01
Job time : 265.5 secs

```
QY      81 Asp 81
      |||
Db      410 GAT 412

RESULT 15
US-09-918-995-26075
; Sequence 26075, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26075
; LENGTH: 458
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(458)
; OTHER INFORMATION: n = A,T,C or G

US-09-918-995-26075
```

```
Alignment Scores:
Pred. No.:      1.64e-54      Length:      458
Score:          387.00      Matches:      76
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches:  0
Query Match:     94.39%      Indels:      0
DB:              10          Gaps:         0
```

US-09-648-310-4 (1-81) x US-09-918-995-26075 (1-458)

```
QY      1 MetAsnValAspHisGluValAsnLeuValGluGluHisArgLeuGlySerLys 20
      |||
Db      231 ATGATCTGGATCAGGAGTTAACTCTTAGTGAGGAAATTCATCGTTGGGTTCAAAA 290
      |||
QY      21 AsnAlaAspGlyLysLeuSerValLysPheGlyValLeuPheArgAspAspLysCysAla 40
      |||
Db      291 AATGCTGATGAAAAGTTAAGCGTGAATTTGGGGTCTCTCTCCGTGATGATAAATGTGCC 350
      |||
QY      41 AsnLeuPheGluAlaLeuValGlyThrLeuLysAlaAlaLysArgArgLysIleValThr 60
      |||
Db      351 AACCTCTTTGAAGCATTTGGTAGGAACCTTAAAGCTGCATAAACGAGGAGATTGTAACA 410
      |||
QY      61 TyrProGlyGluLeuLeuGlnGlyValHisAspValAspLle 76
      |||
Db      411 TATCCAGGAGAGCTGCTTCTGCAAGGTGTTTCATGATGATGTTGACATT 458
      |||
```

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